
WQSRFH

(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Nov 5 09:13:43 1998; MasPar time 2713.32 Seconds
1526.778 Million cell updates/sec

Tabular output not generated.

Title: >US-08-848-439-1
Description: (1-2027) from US08848439.seq
Perfect Score: 2027
N.A. Sequence: 1 GAATTCGGCTTCATGCCTT.....AAAAAAGGCGCGC 2027
Comp: CTTAAGCGGAGTACCGGA.....TTTTTTTTTTCGCGCGC

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 552174 seqs, 1021863385 bases x 2

Post-processing: Minimum Match 0%
Listing first 60 summaries

Database: emb155
1:em_ba 2:em_htg 3:em_hum1 4:em_hum2 5:em_in 6:em_om
7:em_or 8:em_ov 9:em_pat 10:em_pl 11:em_ro
genbank107
Database: 12:gb_ba 13:gb_htg 14:gb_in 15:gb_om 16:gb_ov 17:gb_pat
18:gb_ph 19:gb_pl 20:gb_pr1 21:gb_pr2 22:gb_ro 23:gb_st
24:gb_sts 25:gb_sy 26:gb_un 27:gb_vi

Statistics: Mean 12.049; Variance 7.022; scale 1.716

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1043	51.5	2028	22	MMU8567 Mus musculus secreted	0.00e+00
2	993	49.0	2031	22	AF017989 Mus musculus secreted	0.00e+00
3	959	47.3	1776	22	D50452 Mouse SDF5 mRNA, compl	0.00e+00
4	766	37.8	882	21	AF017986 Homo sapiens secreted	0.00e+00
5	110	5.4	1984	21	AF017988 Homo sapiens secreted	8.64e-40
6	106	5.2	2094	21	AF017987 Homo sapiens secreted	4.01e-47
7	106	5.2	4240	15	BRU8945 Bos taurus frizzled-re	4.01e-47
8	103	5.1	2075	21	AF001900 Homo sapiens secreted	3.93e-45
9	103	5.1	4469	21	AF056087 Homo sapiens secreted	3.93e-45
10	101	5.0	2659	22	MMU8566 Mus musculus secreted	8.29e-44
11	97	4.8	7218	17	156494 Sequence 14 from paten	3.60e-41
12	96	4.7	7218	17	166494 Sequence 14 from paten	1.63e-40
13	83	4.1	2075	16	AF008508 Gallus gallus crescent	4.64e-32
14	60	3.0	2184	21	HSU82169 Human frizzled homolog	1.15e-17
15	60	3.0	106049	13	AC005049 Homo sapiens clone RG0	1.15e-17

16	60	3.0	136389	13	AC005074 Homo sapiens clone RG2	1.15e-17
17	58	2.9	2334	20	HSU43318 Human putative transme	1.84e-16
18	57	2.8	2328	16	AF031830 Gallus gallus 7-transm	7.39e-16
19	56	2.8	2421	22	MMU43321 Mus musculus putative	2.87e-15
20	51	2.5	1881	22	AF054623 Mus musculus frizzled-	2.49e-12
21	48	2.4	1181	16	AF059570 Xenopus laevis secreta	1.32e-10
22	49	2.4	1851	16	AF017177 Xenopus laevis frizzle	3.55e-11
23	49	2.4	10772	14	AF012089 Drosophila melanogaste	3.55e-11
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26	45	2.2	1912	22	RATFRZ2H Rattus norvegicus Dros	6.52e-09
27	42	2.1	1727	16	AF031831 Gallus gallus 7-transm	2.95e-07
28	41	2.0	1923	21	HUMFRIZ Human frizzled gene pr	1.03e-06
29	39	1.9	215	17	I28278 Sequence 5 from patent	1.32e-05
30	38	1.9	4540	22	RATFRZ2H Rattus norvegicus Dros	4.10e-05
31	34	1.7	74371	21	AC005369 Homo sapiens chromosom	4.62e-03
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34	30	1.5	354	14	OFU89259 Oxytricha fallax 57KD	4.02e-01
35	30	1.5	4297	19	ATHSC701 A.thaliana hsc70-1 gen	4.02e-01
36	31	1.5	38262	14	CELK02A2 Caenorhabditis elegans	1.35e-01
37	31	1.5	147898	13	HS1111N9 Human DNA sequence ***	1.35e-01
38	29	1.4	156	24	DM36D7S D. melanogaster STS de	1.17e-00
39	29	1.4	307	14	AF010529 Plasmodium falciparum	1.17e-00
40	28	1.4	400	24	GI3596 human STS SHGC-11851	3.33e+00
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44	28	1.4	1566	21	HUMBCI Homo sapiens mRNA for	3.33e+00
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46	28	1.4	1567	17	I33410 Sequence 2 from patent	3.33e+00
47	28	1.4	1575	17	A13845 H.sapiens PP4 mRNA.	3.33e+00
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51	29	1.4	2028	21	HSU58813 Human polycysticin mRNA	1.17e+00
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57	28	1.4	10934	12	ECAE000479 Escherichia coli K-12	3.33e+00
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59	29	1.4	115641	19	F8K4 Arabidopsis thaliana c	1.17e+00
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ALIGNMENTS

RESULT	1	MMU8567	2028 bp	mRNA	ROD	22-APR-1997
LOCUS		MUS musculus secreted	frizzled related protein	SFRP-2 (Sfrp2)	mRNA,	
DEFINITION		complete cds.				
ACCESSION		U88567				
NID		g1946342				
KEYWORDS		house mouse.				
SOURCE		Mus musculus				
ORGANISM		Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE		1 (bases 1 to 2028)				
AUTHORS		Rattner,A., Hsieh,J.-C., Smallwood,P.M., Gilbert,D.J., Copeland,N.G., Jenkins,N.A. and Nathans,J.				
TITLE		A family of secreted proteins contains homology to the cysteine-rich ligand-binding domain of frizzled receptors				
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 94 (7), 2859-2863 (1997)				
MEDLINE		97250455				
REFERENCE		2 (bases 1 to 2028)				
AUTHORS		Rattner,A., Hsieh,J.-C., Smallwood,P.M., Gilbert,D.J., Copeland,N.G., Jenkins,N.A. and Nathans,J.				
TITLE		Direct Submission				
JOURNAL		Submitted (05-FEB-1997) Molecular Biology and Genetics, HHMI/Johns				

Hopkins University School of Medicine, 725 North Wolfe Street, PCTB
805, Baltimore, MD 21205

FEATURES

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/chromosome="3"
/map="near Fgg"
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OKGOREFRISRSRKLOC"
BASE COUNT 469 a 586 c 480 g 492 t 1 others
ORIGIN

Query Match 51.5%; Score 1043; DB 22; Length 2028;
Best Local Similarity 81.8%; Pred. No. 0.00e+00;
Matches 1558; Conservative 0; Mismatches 312; Indels 34; Gaps 24;

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D 187 GCGTCCCGGCTCGGCTCCCTCGGCCCCCGGGGGTGCCTAGTCACAGATGCCGGGG 246
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Q 387 GCGCAACCTGACGTGTGCGACGGATCGAATACAGAACATCGCGCTGCCCAACCTGT 446
D 427 GGGCCACGAGACCATGAAGGAGTGTGAGCAGCGGGCGGCTGGATTCCGCTGCTCAT 486
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D 1865 TTTTGCAAACTAAATCATGTTAGCTTACCTGCTGATATAGCTAGTGTGACCTGGAAG 1924

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Db 1985 TATATAAATCTTACATCTTGTGTACCTATATAAAAAA 2028
QY 1975 TATATAAATCTTACATCTTGTGTACCTATATAAAAAA 2018

RESULT 2
LOCUS AF017989 2031 bp mRNA ROD \ 21-SEP-1997
DEFINITION Mus musculus secreted apoptosis related protein 1 (Sarpi) mRNA,
complete cds.
ACCESSION AF017989
NID 92415420
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2031)
AUTHORS Meikonyan.H., Chang.W.C., Shapiro.J.P., Mahadevappa.M.,
Fitzpatrick.P.A., Kiefer.M.C., Tomei.D.L. and Umansky.S.R.
TITLE SARPs - a new family of proteins that regulate apoptosis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2031)
AUTHORS Meikonyan.H., Prochazka.V. and Umansky.S.R.
TITLE Direct Submission
JOURNAL Submitted (11-AUG-1997) LXR Biotechnology, Inc., 1401 Marina Way
South, Richmond, CA 94804, USA

FEATURES
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ORIGIN

Query Match 49.0%; Score 993; DB 22; Length 2031;
Best Local Similarity 81.3%; Pred. No. 0.00e+00;
Matches 1522; Conservative 0; Mismatches 313; Indels 36; Gaps 25;

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 QY 1439 AGTTTGAATAGTGCA--ACTGTGACTTGGTGTGGTGTGTTGTTTGT-T-T 1493
 Db 1269 TGGCTTATACCGTGCACTAGTGTGATGTCATGAGGCAATGTTCTTTTGTGTTT 1328
 QY 1494 TGAGTCAG--C-TGATTTTTCATCTCCAC-TGAGTTTGTATACATGCAAAATGCTCA 1549
 Db 1329 TTTCCCTCTGTGCTAAGCTTGTGGTCCAGACTTAGTTGAGATAAGCTGCTCTTA 1388
 QY 1550 ATTTTCTGTGCCCCAACTTGTGGTCAAAACCTGTGAGATAAGCTGCTCTTA 1609
 Db 1389 TCTCAAGTCTTCTCAGTCTCCAGCTGAGAATCGGCATCTAAGTCTTCAAAATTTCTG 1448
 QY 1610 TCTCAACATCTTATCAGCTCCAGACTGAGACTCAGTGTCTAAGTCTTACAAATTCAT 1669
 Db 1449 TGTCTGTTTATGCTCTATGAGCTGTGACCATGTGANGGTTCCCATCCAGTACAGA 1508
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 QY 1728 ACTTCATTTATAGAGCACATTAACCATTTCT-ATAGCATGATTTCTTCAAGTAAAG 1786
 Db 1568 GTGAATACAGTCTATAAATGAGGAGTATTTTAAAGCTTTCTTTAAACATCTTTTAATTC 1627
 QY 1787 GCAAA-AGA-TATA-AATTTTAAATGACTTGAG--TAGTTTAAAGCTTGTTTAAAA-C 1840
 Db 1628 AATTTTAAATCAATTTTGTGAAACTAAATCATTTAGCTTACCTGTATATACAGTAG 1687
 QY 1841 A-TTCTTACTTAACCTTTGCA-AATTAACCCATTTAGCTTACCTGTATATACATAG 1898
 Db 1688 TAGTTGACCTGGAAGAGTGTAAAAATATTTGCTTTAACCCAGACTGTAAATATTCAGAT 1747
 QY 1899 TAGTTTACCTTTTAAAGTGTAAAAATATTTGCTTTAACCAACACTGTAAATATTCAGAT 1958
 Db 1748 AAACATTAATATCTTTGTATATAAATTT 1776

QY 1959 AAACATTATATTCTT-GTATATAAACTTT 1986

RESULT 4 AF017986 882 bp mRNA PRI 21-SEP-1997
 LOCUS Homo sapiens secreted apoptosis related protein 1 (SARP1) mRNA,
 partial cds.
 ACCESSION AF017986
 NID 92415414
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 882)
 AUTHORS Melkonian, H., Chang, W.C., Shapiro, J.P., Mahadevappa, M.,
 Fitzpatrick, P.A., Kiefer, M.C., Tomei, D.L., and Umansky, S.R.
 SARPs - a new family of proteins that regulate apoptosis
 TITLE Unpublished
 JOURNAL 2 (bases 1 to 882)
 AUTHORS Melkonian, H., Prochazka, V. and Umansky, S.R.
 TITLE Direct Submission
 JOURNAL Submitted (11-AUG-1997) LXR Biotechnology, Inc., 1401 Marina Way
 South, Richmond, CA 94804, USA
 FEATURES
 Location/Qualifiers
 source 1..882
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 ANLOLCHIEIQNRLPNLGHETMEVLEQAGAWIPLVMKQCHPDKFKLCSLPAPV
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 BASE COUNT 167 a 318 c 233 g 163 t 1 others
 ORIGIN

Query Match 37.8%; Score 766; DB 21; Length 882;
 Best Local Similarity 97.6%; Pred. No. 0.00e+00;
 Matches 841; Conservative 0; Mismatches 10; Indels 11; Gaps 4;
 Db 29 CTGGCTCATTTGCTCCCGGGTGGAGAGCCCCCGGAGCTGCGCGGGCTTGAGGCG 88
 QY 19 CTAGCTCATTTGCTCCCGGGTGGAGAGCCCCCGGAGCTGCGCGGGCTTGAGGCG 78
 Db 89 CTCGCCCGGCTGCTCCCGGTGTCGGCTTCTCCGCGCCCGCCAGCCCGGCTGCCAGC 148
 QY 79 CTCGCCCGGCT--CTTCCCGGTGTCGGCTTCTCCGCGCCCGCCAGCCCGGCTGCCAGC 136
 Db 149 TTTTCGGGGCCCCGAGTGCACCCAGGAGAGAGAGCGGGCCCGGACAAAGTTCGAATCC 208
 QY 137 TTTTCGGGGCCCCGAGTGCACCCAGGAGAGAGAGCGGGCCCGGACAAAGTTCGAATCC 196
 Db 209 GGCGGCTCGGCCCTTACAGCTCCG-TCCCTCTACCCCTTAGGGGTGCGCG--CCACGA 265
 QY 197 GGCGGCTCGGCCCTTCCCGGCTCCGCTCCCTCTGCGGCTCGGGGTGCGCGCCACGA 256
 Db 266 TGCTGAGGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 325
 QY 257 TGCTGAGGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 316
 Db 326 CGGCGCGGGGCTCTTCTCTCTTTGGCCAGCCGAGCTTCTCTACAGGCGGAGCAATTCGA 385
 QY 317 CGGCGCGGGGCTCTTCTCTTTGGCCAGCCGAGCTTCTCTACAGGCGGAGCAATTCGA 376
 Db 386 AGCCCATCCGGGCCAACCTGCAGCTGTGCCAGGCGATCGAATACAGAACATCGCGGCTGC 445

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BASE COUNT 484 a 598 c 631 g 381 t

ORIGIN

Query Match 5.2%; Score 106; DB 21; Length 2094;

Best Local Similarity 71.8%; Pred. No. 4.01e-47;
Matches 249; Conservative 0; Mismatches 89; Indels 9; Gaps 5;

Db 452 CTTCTACACCAAGCCACCTCAGTGGTGACATCCCGCGGACCTCGGCTGTGCCACAA 511
QY 351 CTTCTCTACAGCGCAGCAATTCGAAGCCCATCCGGCCACCTCGCTGTGCCACGS 410
Db 512 CTTGGGCTACAGAGATGGTGTGCCCAACCTGTGGAGCAGGACCATGCGCGAGGT 571
QY 411 CATCGAATACCAAGACATCGGCTGCCCAACCTGTGGCCACGAGACCATGAAGGAGT 470
Db 572 GAAGCAGCAGCGCAGCAGTGGTGGCTGCTGTCAACAGAACTGCCACGCCGCCACCA 631
QY 471 GCTGGAGCAGCGCGGCTGTGATCCGCTGGTCATGAAGCAGTGCCACCGGACACCA 530
Db 632 GGTCTTCTCTCTGCTCTCGCGCCCTCTGCGCT-G--GACCG-G-C---CCATCTA 682
QY 531 GAAGTTCCTGCTGCTCTTCGCGCCCTCTGCGCTGCTGATGACCTAGACGAGACATCA 590
Db 683 CCGGTGTGCTGCTGCTGCGAGCGCTGCGGACCTGCTGCGAGCCGGTTCATGCACTTT 742
QY 591 GCGATGCCACTGCTGCTGCTGAGTGAAGACCGCTGCGCCCGGTTCATGTCGCCCTT 650
Db 743 CGGCTTCTACTGGCGCGGAGATGCTTAAGTGTGACAAGTTCCCGGAGG 789
QY 651 CGGCTTCCCTGCGCGGACATGCTTGAGTGCAGCCGTTTCCCGCAGG 697

RESULT 7 BTU85945 4240 bp mRNA MAM 21-AUG-1997
LOCUS Bos taurus frizzled-related protein Frza mRNA, complete cds.
DEFINITION U85945
ACCESSION 92337936
NID
KEYWORDS Bos taurus.
SOURCE Bos taurus.
ORGANISM Bos taurus.
REFERENCE Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
AUTHORS Vertebrata; Mammalia; Euthera; Artiodactyla; Ruminantia; Pecora;
TITLE Bovidae; Bovidae; Bovinae; Bos.
JOURNAL Duplaa, C. and D'Amore, P.A.
REFERENCE 1 (bases 1 to 4240)
AUTHORS Identification and cloning of a novel secreted form of mammalian
TITLE frizzled: evidence to suggest a role in the control of growth and
JOURNAL differentiation
REFERENCE 2 (bases 1 to 4240)
AUTHORS Duplaa, C. and D'Amore, P.A.
TITLE Direct Submission
JOURNAL Submitted (20-JAN-1997) INSERM U441, AV du Haut Leveque, Pessac
33600, France
FEATURES Location/Qualifiers
source 1..4240
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198..1124
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IAMTPNATEASKPGQTTVPCPDNELKSEAIIIEHLCASEFALRMKIKVKKENGDKK
IYVKKKPLKGLPIKKDLKLVLYLKNAGADPCCHOLDNLSHHFLMGRKVKSOYLLT
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sig_peptide 210..263

misc_feature 966..968

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BASE COUNT 1015 a 1073 c 1112 g 1040 t

ORIGIN

Query Match 5.2%; Score 106; DB 15; Length 4240;

Best Local Similarity 71.4%; Pred. No. 4.01e-47;
Matches 252; Conservative 0; Mismatches 92; Indels 9; Gaps 5;

Db 329 CTTCTACACCAAGCCAGTGGTGGACATCCCGGAGACCTCGGCTGTGCCACAA 388
QY 351 CTTCTCTACAGCGCAGCAATTCGAAGCCCATCCCGCCCACTGCGCTGTGCCACG 410
Db 389 CTTGGGCTACAGAGATGGTGTGCCCAACCTGTGGAGCAGGACCATGCGCGAGGT 448
QY 411 CATCGAATACCAAGACATCGGCTGCCCAACCTGTGGCCACGAGACCATGAAGGAGT 470
Db 449 GAAGCAGCAGCGCAGCAGTGGTGGCTGCTCAACAGAACTGCCACATCGGCACCA 508
QY 471 GCTGGAGCAGCGCGGCTTGGATCGGCTGCTCATGAAGCAGTGCACCCGACACCA 530
Db 509 GGTCTTCTCTGCTGCTCTTCGCGCCCTCTGCGT-G--GACCG-G-C---CCATCTA 559
QY 531 GAAGTTCCTGCTGCTCTTCGCGCCCTCTGCGCTGCTGATGACCTAGACGAGACATCA 590
Db 560 CCGGTGTGCTGCTGCTGCGAGCGCTGCGGACCTGCTGGAGCGGTCATGCACTTT 619
QY 591 GCGATGCCACTGCTGCTGCTGAGTGAAGACCGCTGCGCCCGGTTCATGTCGCCCTT 650
Db 620 CGGCTTCTACTGGCGCGGAGATGCTCAAGTGCAGCAAGTTTCCCGAGGCGGAG 672
QY 651 CGGCTTCCCTGCGCGGACATGCTTGAGTGCAGCCGTTTCCCGCAGGACAAAG 703

RESULT 8 AF001900 2075 bp mRNA PRI 25-JUN-1997
LOCUS Homo sapiens secreted frizzled-related protein mRNA, complete cds.
DEFINITION AF001900
ACCESSION 92213818
NID
KEYWORDS human.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
AUTHORS Vertebrata; Mammalia; Euthera; Primates; Catarrhini; Homnidae;
TITLE Homo.
JOURNAL 1 (bases 1 to 2075)
AUTHORS Finch, P.W., He, X., Kelley, M.J., Uren, A., Schaudies, R.P.,
REFERENCE 2 (bases 1 to 2075)
AUTHORS Popescu, N.C., Rudikoff, S., Aaronson, S.A., Varnus, H.E. and
TITLE Finch, P.W., Aaronson, S.A. and Rubin, J.S.
JOURNAL - Direct Submission
REFERENCE 3 (bases 1 to 2075)
AUTHORS Submitted (30-APR-1997) LCMB, DBS/NCI, 9000 Rockville Pike,
TITLE Bethesda, MD 20892, USA
JOURNAL 1..2075
/organism="Homo sapiens"
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BASE COUNT 473 a 596 c 626 g 380 t
ORIGIN

Query Match 5.1%; Score 103; DB 21; Length 2075;
Best Local Similarity 73.5%; Pred.No. 3.93e-45;
Matches 161; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Db 449 CTTCTACCAAGCCACCTCAGTGCCTGCGGACATCCCGCGGACCTGGCGTGTGCCACAA 508
QY 351 CTTCTCTACAAGCGCAGCAATTCGAAGCCATCCCGGCCAACCTGCAGCTGTGCCACGG 410

Db 509 CGTGGGCTACAAGAAGATGGTGTGCGCCACCTGCTGGAGCAGCAGACCATGGCGGAGGT 568
QY 411 CATCGAATACCAAGCAACATGGCGCTGCGCCACCTGCTGGCGCCGCGTGTGCTCGA 530

Db 569 GAAGCAGCAGCGCAGCAGCTGGGTGCGCCCTGCTCAACAAGAACTGCCACGCGGGACCCA 628
QY 471 GCTGAGCAGCGCGCGCTTGGATCCCGCTGGTGCATGAAGCAGTGCACCGCGGACACAA 530

Db 629 GGTCTTCTCTGCTGCTTTCGCGCCGCGTGTGCTGTGGA 667
QY 531 GAAGTTCTGCTGCTCTTCGCGCCGCGTGTGCTGTGGA 569

RESULT 9
LOCUS AF056087 4469 bp mRNA PRI 08-APR-1998
DEFINITION Homo sapiens secreted frizzled related protein mRNA, complete cds.
ACCESSION AF056087
NID 93033550
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 4469)
AUTHORS Zhou,Z. and Wang,J.
TITLE Upregulation of human secreted Frizzled homologue in apoptosis and its down regulation in breast tumors
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 4469)
Zhou,Z. and Wang,J.
TITLE Direct Submission
JOURNAL Submitted (29-MAR-1998) Radiohemmet Research Laboratory, CKK, Karolinska Institute, Solnavagen, Stockholm S-171 76, Sweden
FEATURES
source Location/Qualifiers
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303..1244
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CDS

Query Match 5.1%; Score 103; DB 21; Length 2075;
Best Local Similarity 73.5%; Pred.No. 3.93e-45;
Matches 161; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Db 449 CTTCTACCAAGCCACCTCAGTGCCTGCGGACATCCCGCGGACCTGGCGTGTGCCACAA 508
QY 351 CTTCTCTACAAGCGCAGCAATTCGAAGCCATCCCGGCCAACCTGCAGCTGTGCCACGG 410

Db 509 CGTGGGCTACAAGAAGATGGTGTGCGCCACCTGCTGGAGCAGCAGACCATGGCGGAGGT 568
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Db 569 GAAGCAGCAGCGCAGCAGCTGGGTGCGCCCTGCTCAACAAGAACTGCCACGCGGGACCCA 628
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Db 629 GGTCTTCTCTGCTGCTTTCGCGCCGCGTGTGCTGTGGA 667
QY 531 GAAGTTCTGCTGCTCTTCGCGCCGCGTGTGCTGTGGA 569

RESULT 10
LOCUS MMU88566 2659 bp mRNA ROD 22-APR-1997
DEFINITION Mus musculus secreted frizzled related protein sFRP-1 (Sfrp1) mRNA, complete cds.
ACCESSION U88566
NID g1946340
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 2659)
AUTHORS Rattner,A., Hsieh,J.-C., Smallwood,P.M., Gilbert,D.J., Copeland,N.G., Jenkins,N.A. and Nathans,J.
TITLE A family of secreted proteins contains homology to the cysteine-rich ligand-binding domain of frizzled receptors
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (7), 2859-2863 (1997)
MEDLINE 97250455
REFERENCE 2 (bases 1 to 2659)
Rattner,A., Hsieh,J.-C., Smallwood,P.M., Gilbert,D.J., Copeland,N.G., Jenkins,N.A. and Nathans,J.
AUTHORS Copeland,N.G., Jenkins,N.A. and Nathans,J.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-1997) Molecular Biology and Genetics, HHMI/Johns Hopkins University School of Medicine, 725 North Wolfe Street, PCTB 805, Baltimore, MD 21205
FEATURES
source Location/Qualifiers
1..2659
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="8"
/map="between Plat and Fgfr1"
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CDS
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BASE COUNT 645 a 738 c 719 g 553 t 4 others
ORIGIN

Query Match 5.0%; Score 101; DB 22; Length 2659;

Best Local Similarity 73.1%; Pred. No. 8.29e-44;

Matches 150; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

Db 406 CTTCTACCAAGCCCGCCGAGTCGCTGACATCCCGTGACCTGCGAGCAGACCATGGCAGAGGT 465

QY 351 CTTCTCTACAGCGCAGCAATTCAGAGCCATCCCGGCCAACCTCGCAGCTGTGCCAGGG 410

Db 466 CGTGGCTACAGAGATGCTGCTGCCACCTCTGCGAGCAGCAGACCATGGCAGAGGT 525

QY 411 CATCGAATACAGAACATCGCGCTGCCAACCTCTGCGGCCACGAGACCATGAAGAGGT 470

Db 526 GAAGCAGCAGCAGCAGCAGCTGCTCAACAAGAACTGCCACATGGCAGCCCA 585

QY 471 GCTGGAGCAGCGCGCGCTGGATCCCGCTGCTCATGAAGCAGTGCACCCGAGACCAA 530

Db 586 GGTCTTCTCTGCTGCTCTGCGCGCGCTGCTGCTGGA 624

QY 531 GAAGTCTCTGCTGCTCTGCGCGCGCTGCTGCTGGA 569

RESULT 11

LOCUS 166494 7218 bp DNA PAT 23-DEC-1997

DEFINITION Sequence 14 from patent US 5670367.

ACCESSION 166494

NID 92724471

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 7218)

AUTHORS Dörner, F., Scheiflinger, F. and Falkner, F. Gunter.

TITLE Recombinant fowlpox virus

JOURNAL Patent: US 5670367-A 14 23-SEP-1997;

FEATURES Location/Qualifiers

source 1..7218

BASE COUNT 1944 a 1491 c 1486 g 1929 t 368 others

ORIGIN

Query Match 4.8%; Score 97; DB 17; Length 7218;

Best Local Similarity 1.4%; Pred. No. 3.60e-41;

Matches 5; Conservative 224; Mismatches 132; Indels 0; Gaps 0;

Db 1061 TGGCATYY 1120

Cp 1111 TGGCTTGAACCTCTCTGCGCCCTTCCACCGCTTCCAGGATGATCACCAGCTCCC 1052

Db 1121 YY 1180

Cp 1051 CACCCCTTTCTGTCCTCCTCCTGATGAGGCGGTGATGCTGCTCCTCCTCAGAGG 992

Db 1181 YY 1240

Cp 991 TGCACCTCAAGCTCTCTTGGACACACACCGCAGTATTTCTCAGGTCCTTTCCGACACAC 932

Db 1241 YY 1300

Cp 931 CGTTCACCTGTAATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 872

Db 1301 YY 1360

Cp 871 TGTAGGTTATCTCTCTCCTTATTTTTCAGTGCAAAATCATTTTACAAAGCGTTTCCA 812

Db 1361 YY 1420

Cp 811 TTATGCTGCTGCTATCATCATTTTATTTTTCAGGCTTTCATACACCTTTGGAGCTTCT 752

Db 1421 Y 1421

Handwritten: New to find w/ virus

Cp 751 C 751

RESULT 12

LOCUS 166494 7218 bp DNA PAT 23-DEC-1997

DEFINITION Sequence 14 from patent US 5670367.

ACCESSION 166494

NID 92724471

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 7218)

AUTHORS Dörner, F., Scheiflinger, F. and Falkner, F. Gunter.

TITLE Recombinant fowlpox virus

JOURNAL Patent: US 5670367-A 14 23-SEP-1997;

FEATURES Location/Qualifiers

source 1..7218

BASE COUNT 1944 a 1491 c 1486 g 1929 t 368 others

ORIGIN

Query Match 4.7%; Score 96; DB 17; Length 7218;

Best Local Similarity 0.6%; Pred. No. 1.63e-40;

Matches 2; Conservative 224; Mismatches 130; Indels 0; Gaps 0;

Db 1065 ATYYY 1124

QY 3 ATTCGGCCTTACGCTAGCTCATTCCTCCCGGTCGGAGCCCGCCGAGCTGGC 52

Db 1125 YY 1184

QY 63 CGCGGCTTGCAGCCCTCGCGCGCTCTCCCGGTCTCCCGCTCTCCGCGCCACG 122

Db 1185 YY 1244

QY 123 CGCGGCTGCCAGCTTTTCGGGCGCCCGAGTCGCACCGACGAGAGCGGCGGGA 182

Db 1245 YY 1304

QY 183 CAAGCTGAACCTCGCGCGCTCGCGCTTCCCGGCTCCCGCTCTGCTGCTGCTGCTGCT 242

Db 1305 YY 1364

QY 243 TCGCGCGCCAGATGTCAGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302

Db 1365 YY 1420

QY 303 CTGCTGCTGCGCTCGCGCGCTCTCTCTCTTGGCCAGCCGAGCTTCTCTCT 358

RESULT 13

LOCUS AF006508 2075 bp mRNA VRT 30-JUN-1997

DEFINITION Gallus gallus crescent mRNA, complete cds.

ACCESSION AF006508

NID 92226371

KEYWORDS

SOURCE chicken.

ORGANISM Gallus gallus

Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Archosauria; Aves; Neognathae; Galliformes;

Phasianidae; Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 2075)

AUTHORS Pfeffer, P.L., Izpisua-Belmonte, J.C. and De Robertis, E.M.

TITLE crescent

JOURNAL Int. J. Dev. Biol. (1997) In press

REFERENCE 2 (bases 1 to 2075)

AUTHORS Pfeffer, P.L., Izpisua-Belmonte, J.C. and De Robertis, E.M.

TITLE Direct Submission

JOURNAL Submitted (28-MAY-1997) IMP, Dr. Bohrgasse 7, Vienna 1030, Austria

FEATURES Location/Qualifiers

source 1..2075

/organism="Gallus gallus"


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* as runs of N as a convenience only. When sequencing is complete,
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Db	2267	GGTCGTTGCGGTGGGCACCGGGCGCGAGTCGACGGAGTGCGGCCAGCCGAAGTTGAAC	2326	
Cp	706	GGTCGTTGCTGGGGGAAACGGTGCACCTAAGCATGTGGGCCGAGGGGAAGCCGAAGG	647	
Db	2327	GTCTCCATGATGGCGCGGCACGCGCGCTGCTGCACATGGCGCGCGAGCGGGAA	2386	
Cp	646	CGSACATACCGGGGGCGACGGTCTCTCACCTGCACGACGAGTGGCATGGCTGGA	587	
Db	2387	TGGGCGCTGAGACCTGGTCGTGTGCATATGGGCGCGCTAGAGGAGCACAGGAAGACGCA	2446	
Cp	586	TGCTCTCGCTAGTTCATCGAGCGACAGGGGGCGAAGCGACGACAGAACTCTTTGG	527	
Db	2447	GTGTGGCTGTGGCAGCGGTACTGCACAGCGCGCGAACTCCGCTAGCTCGGCAGCCGCT	2506	
Cp	526	TGTCCGGGTGGCACTGCTTCATGACACGGGGATCCAAAGCGCGGCCCTGCTCCAGCACT	467	
Db	2507	CGCCCTGCCACAGTGTGGCCCGACAGGTTGGGCGATGCGGGTCAGGTTGTAGCCGATGCCGC	2566	
Cp	466	CTTCATGGTCTGTCGGCCGACAGGTTGGGCGACCGCATGTTCTGTGTTATTCGATGCCGT	407	
Db	2567	GGCACA	2572	
Cp	406	GGCACA	401	

RESULT	16
LOCUS	AC005074 136389 bp DNA HTG 12-JUN-1998
DEFINITION	Homo sapiens clone RG208H19; HTGS phase 1, 1 unordered pieces.
ACCESSION	AC005074
NID	93212917
KEYWORDS	HTG; HTGS_PHASE1.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 136389) Waterston,R.H. The sequence of Homo sapiens clone Unpublished 2 (bases 1 to 136389) Waterston,R.H. Direct Submission Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis MO 63108, USA

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*** WARNING: Phase 1 High Throughput Genome Sequence ***
***
* This sequence is unfinished. It consists of 1 contigs for
* which the order is not known; their order in this record is
* arbitrary. In some cases, the exact lengths of the gaps
* between the contigs are also unknown; these gaps are presented
* as runs of N as a convenience only. When sequencing is complete
* the sequence data presented in this record will be replaced
* by a single finished sequence with the same accession number.
* 1. 136389: contig of 136389 bp in length.
* Location/Qualifiers
FEATURES

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FEATURES

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source      1. .136389
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BASE COUNT  33882 a 32574 c 33810 g 36123 t
ORIGIN
Query Match      3.0%; Score 60; DB 13; Length 136389;
Best Local Similarity 59.8%; Pred. No. 1.15e-17;
Matches 183; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

Db 52669 GGTGGTTGGCGTGGGCGAGCCGGCGCAGTCGAGCGAGTCCGCCACGCGAAGTTCAACT 52728
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Cp 706  GGTCGTTGTCTCTGGGGAAACGGTGCACCTCAAGCATGTGGGCCACAGGGAAGCCGAAG 647
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Db 52729 GCTCCATGATGGCGCGCAGCGCAGCGCGCGCTGCTCGCACATGGCGCCGCGAGCGGGAA 52788
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Cp 646  CGGACATACCGGGGCGCAGCGGTCTTCCACTGCACGACGACGAGTGGCATGGCTGA 587
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Db 52789 TGGCGCTGAGACCTGGTCGGTGCACATGGGCGCGTAGAGCGAGCAGACAGGAACGCGA 52848
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Cp 586  TGGTCTCGTCTAGGTCTATCAGAGCAGCGGGGCGAAGACGCGACGACAGCACTTCTGG 527

Db 52849 GGTGGCTGTGGCAGCCGTACTGTACACAGGGCGCGCAACTCCGCTAGCTCGGACGCGCCT 52908
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Cp 526  TGTCGGGTGGCACTGCTTTCATGACACAGGGGATCCAGGGCGGGCGCTGCTCCAGCACT 467
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Db 52909 CGCCCTCGCAGCTGTGGCCCGACGAGTTGGGCATGCGGGTTCAGGTTGTAGCCGATGCCGC 52968
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Cp 466  CTTTCATGGTCTCGTGGCCCGCAGAGTTGGGCGACCGGCATGTTCTGGTATTGATGCCGT 407
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Db 52969 GGCACA 52974
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Cp 406  GGCACA 401
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RESULT	17	HSU03318	2334 bp	mrna	PRI	24-FEB-1996
LOCUS		Human putative transmembrane receptor (frizzled 5)				complete
DEFINITION		cds.				
ACCESSION		U43318				
NID		g1151251				
KEYWORDS		human.				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1-(bases 1 to 2334)				
AUTHORS		Wang Y., Macke, J.P., Abella, B.S., Andreasson, K., Worley, P., Gilbert, D.J., Copeland, N.G., Jenkins, N.A. and Nathans, J.				
TITLE		A large family of putative transmembrane receptors homologous to the product of the <i>Drosophila</i> tissue polarity gene <i>frizzled</i> J.-Biol. Chem. 271(8), 4468-4476 (1996)				
JOURNAL		96224032				
MEDLINE		2 (bases 1 to 2334)				
AUTHORS		Abella, B., Wang, Y., Macke, J.P. and Nathans, J.				
TITLE		Direct Submission				
JOURNAL		Submitted (14-DEC-1995)				
AUTHORS		Jeremy Nathans, Molecular Biology and Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street, Baltimore, MD 21205				

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AVCYQPSFADERTFATFWGLNSVLCFISTVTATFLDMDFRYPERPILFLSA
CLVSLGFLVRLVGVHAFVACSRHNIHETTPALCTIVFLLYFFFGMASSIVWY
ILSTUTLAAKMGNEAGIGQIFHLAHLWILSVKSTALASSVDGDPVAGICVY
GNQNLNRLRVLGLVLLVLLVGLFLLAGVSLFRSVIKOGGTTDKLEKLMIRI
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BASE COUNT 356 a 803 c 736 g 439 t
ORIGIN
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Query Match 2.9%; Score 58; DB 20; Length 2334;
Best Local Similarity 59.9%; Pred. No. 1.84e-16;
Matches 175; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

Db 439 TGTGCGCGGCATCGGTACAGCTGACGACATGCCCAACCAAGTGAACACGACAGC 498
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Qy 401 TGTGCGCGGCATCGGTACAGCTGACGACATGCCCAACCAAGTGAACACGACAGC 460
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Db 499 AGGACGAGCGGCTGGAGTGGACAGTGTGGCCGTGGTGGAGATCCATGCTGC 558
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Qy 451 TGAAGAGTGTGGAGAGCGCGGCTGGATCCCGTGGTGTATGAGCAGTGCAC 520
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Db 559 CGGACCTCGGTTTCCTATGATATGATACGCCATCTGTGCCGACTACCA 618
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Qy 521 CGGACCAAGAAGTCTGTGCTGCTGCTGCGCCGCTGCTGCTGCTGCTGCTG 580
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Db 619 AGCCGCTCGCGCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 678
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Qy 581 AGACCATCAGCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 640
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Db 679 TCCGCGCTACGGCTTCGCCGCTGCGCGGATGAGTGGACGCGCTCC 730
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Qy 641 TGTCCGCTCGGCTCGCGCTGCGCGGATGAGTGGACGCGCTCC 692
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RESULT 18
LOCUS AF031830 2328 bp mRNA VRT 02-DEC-1997
DEFINITION Gallus gallus 7-transmembrane protein frizzled-1 (Fz-1) mRNA,
nuclear gene encoding mitochondrial protein, complete cds.
ACCESSION AF031830
NID g2655273
KEYWORDS chicken.
SOURCE Gallus gallus
ORGANISM Gallus gallus
REFERENCE 1 (bases 1 to 2328)
AUTHORS Neognathae; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
Kengaku,M., Twombly,V. and Tabin,C.
TITLE Expression of Wnt and Frizzled genes during chick limb bud
development
JOURNAL Cold Spring Harb. Symp. Quant. Biol. (1997) In press
REFERENCE 2 (bases 1 to 2328)
AUTHORS Kengaku,M. and Tabin,C.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-1997) Genetics, Harvard Medical School, 200
Longwood Ave., Boston, MA 02115
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Location/Qualifiers
/organism="Gallus gallus"
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/tissue_type="limb bud"
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protein"
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FQWEDTLECEFPVHGAGELCVQNASERGTPTPALPRESWTSNPHRGAGGSGPGE
ANGRSPRALKVSILNLYRFLGKDCAPCEPRGLYMTFGPELRFRTWIGWS
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AEDGSRTVAQGTKEGCTILFMILYFFGMASIMWVILSLTWFLAAGMKGHEATEAN
SOYFHLAAWAPAKTITILALGOVDLGSVCFVGINNVDALRGFLVLAFLVFLFI
GTSFLLAGVSLFRITIMKHDTGKTEKLEKLMVRIGFISVLYTVPAIVTACIYEYEQ
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BASE COUNT 394 a 732 c 737 g 463 t
ORIGIN

Query Match 2.8%; Score 57; DB 16; Length 2328;
Best Local Similarity 62.2%; Pred. No. 7.29e-16;
Matches 183; Conservative 0; Mismatches 108; Indels 3; Gaps 2;

Db 439 GCTGTGCACAGACATCGCTTACACACGACACCATCATGCCCAACCTGCTGGGCCACACCAA 498
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Qy 399 GCTGTGCCACGCGCATCGAATACCAACAATCGCGCTGCCCAACCTGCTGGGCCACGAGAC 458
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Db 499 CCAGGAGGACGGGGCTGGAGGTGCACAGTTCTACCGCTGGTGAAGGTGCAGTGTCT 558
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Qy 459 CATGAAGGAGGTGCTGGAGAGCGCGGCTTGGATCGCGTGCATGAAGACAGTGC 518
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Db 559 GGCACCACTGAAGTCTTCCCTGCTCTCATGTACCGCCCGGCTGCACCG-TG--CTGGA 615
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Qy 519 CCGGACACCAAGAAGTTCCTGCTGCTCTTCGCCCGGCTGCCTCGATGACTAGA 578
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Db 616 GCAGCCCTGCGCGCTGCGGCTCTCTTTGAGAGCGCGCGCCGAGGCGGAGGCGCT 675
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Qy 579 CGAGACCATCAGCATCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 638
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Db 676 CATGAACAGTTCGCTTCCAGTGGCCGACACGCTGCTGCTGCTGCTGCTGCTGCTGCT 729
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Qy 639 CATGTCGCTTCCGCTTCCCGTGGCCGACATGCTTGAGTGGCAGCGCTTCC 692
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RESULT 19
LOCUS MMU43321 2421 bp DNA ROD 24-FEB-1996
DEFINITION Mus musculus putative transmembrane receptor (frizzled 8) gene,
complete cds.
ACCESSION U43321
NID g1151259
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 2421)
AUTHORS Wang,Y., Macke,J.P., Abella,B.S., Andreasson,K., Worley,P.,
Gilbert,D.J., Copeland,N.G., Jenkins,N.A. and Nathans,J.
TITLE A large family of putative transmembrane receptors homologous to
the product of the Drosophila tissue polarity gene frizzled
JOURNAL J. Biol. Chem. 271 (8), 4468-4476 (1996)
MEDLINE 96224032
REFERENCE 2 (bases 1 to 2421)
AUTHORS Abella,B., Wang,Y., Macke,J.P. and Nathans,J.
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1995) Jeremy Nathans, Molecular Biology and
Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street,
Baltimore, MD 21205
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Location/Qualifiers
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GELCVGQNTSDKGTPTPSLLPEFNTSGOHGGVGRGYPGGAGTVERKGFSPRALR
VSYLNVHFLGKEKDAGACEPKVYGLMYFGEELRFSRTWTGINSVLCCASTLFTVL
TVLNDPREISPERPIISUGCYTAVAYIAAGFLLEDRVCKNKAEDGATFAVGT
NKEGCTIFPMYLIFFSMASSIIWWILSLTSLAAGMKWGHAEIANSQDFHAAWAP
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BASE COUNT      337 a   602 c   575 g   367 t
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Query Match      2.5%; Score 51; DB 22; Length 1881;
Best Local Similarity 61.2%; Pred. No. 2.49e-12;
Matches 180; Conservative 0; Mismatches 111; Indels 3; Gaps 3;

Db 351 GCTGTGCACGACATGCGGTACACACAGACCATCATGCCCAACCTGCTGGGCCACAGAA 410
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QY 399 GCTGTGCACGGCATGAATACAGAACATCGCGCTGCCCAACCTGCTGGGCCACGAGAC 458
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Db 471 CGCGAGCTCAAGTTCCTCTGTGCTCCATGTACGGCGCTGTGTGCACCG-T-AC-TGGA 527
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Db 588 CATGAACAAGTTCGGCTTCAGTGGCCAGACACACTCAAGTGGAGNAGTTCCTCC 641
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QY 639 CATGTCGCGCTTCGGCTTCCTCCCTGGCCCGACATGCTTGAGTGCAGCGCTTCTCC 692

RESULT 21
LOCUS      AF059570      1181 bp      mRNA      VRT      28-APR-1998
DEFINITION Xenopus laevis secreted Xwnt8 inhibitor sizzled (s21) mRNA,
            complete cds.
ACCESSION  AF059570
NID        g3089550
KEYWORDS   African clawed frog.
SOURCE     Xenopus laevis
            Eukaryota; Metazoa; Chordata; Vertebrata; Amphibia; Batrachia;
            Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus.
REFERENCE  1 (bases 1 to 1181)
AUTHORS   Salic,A.N., Kroll,K.L., Evans,L.M. and Kirschner,M.W.
TITLE     Sizzled: a secreted Xwnt8 antagonist expressed in the ventral
            marginal zone of Xenopus embryos
JOURNAL   Development 124 (23), 4739-4748 (1997)
MEDLINE   98088686
REFERENCE  2 (bases 1 to 1181)
AUTHORS   Salic,A.N., Kroll,K.L., Evans,L.M. and Kirschner,M.W.
TITLE     Direct Submission
JOURNAL   Submitted (14-APR-1998) Cell Biology, Harvard Medical School, 240
            Longwood Ave, Boston, MA 02115, USA
FEATURES   Location/Qualifiers
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gene

CDS

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GGGAFCPCOCRAPWSVSHERHLYNRKTGIQANCALPCNFFFSDDERAFTVF
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STVALSLVDGDGVAGICVGNOSLDNLGRFLTPLYTYPVAVVVACLFEQHNRPWEATHCP
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SQV"

BASE COUNT 403 A 772 C 779 G 467 T

ORIGIN

Query Match 2.8% ; Score 56; DB 22; Length 2421;
Best Local Similarity 59.4%; Pred. No. 2.87e-15;
Matches 177; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

Dbb 306 TGCGGTGTGCAAGGCATCGGTTCACAAGTACACTTACATGCCAACCATTTCAACCACG 365
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Qy 395 TGAGCTGTGCCAGCAGTCGATATCACAGAACATGCGGCTGCCCAACCTGCTGGCCCAG 454
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Db 366 ACACGCAAGATGAGCGGSCCTAGAGGTGCACCAAGTTTTGGCGCTGGTGAGATACAGT 425
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Qy 455 AGACGATGAAGGAGGTGCTGGACGAGCGCGCCTTGATGCCGCTGGTCATGAAGCAGT 514
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Db 426 GTCTCCGAGCCTCAGTCTTTCTGTGTGATGATGATACAGCCCCATCGCTGGAGGACT 485
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Qy 515 GCCACCCGGACACCAAGATTCTGTGCTGCTCTTCGCCCCCGCTGCTGCTGATGACC 574
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Db 486 ACAAGAAGCCTCTGCCGCTGTGCTGTGTAAGCGCAAGCGCGCTGGCGCG 545
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Qy 575 TAGACAGACCATCAGCCATGCCATCGCTGCTGGCTGACAGGAGTAGAGCGCTGCGCCC 634
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Db 546 CGTCAATGCCCEAGTACGGCTTGTGGCTGACCCGATCGCTGCGATCGGTTGCC 603
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Qy 635 CGTCAATGCCCEAGTACGGCTTGTGGCTGACCCGATCGCTGCGATCGGTTGCC 692
|||||

RESULT 20

LOCUS AF054623 1881 bp mRNA ROD 08-APR-1998

DEFINITION Mus musculus frizzled-1 mRNA, complete cds.

ACCESSION AF054623

NID 93025755

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1881)

REFERENCE Xu, L., Muragaki, Y., Olsen, B. and Li, Y.
AUTHORS Direct Submission
TITLE Submitted (18-MAR-1998) Cell Biology, Harvard Medical School, 220
JOURNAL Longwood Ave., Boston, MA 02115, USA

FEATURES Location/Qualifiers
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/strain="C57BL"
/db_xref="taxon:10090"
/dev_stage="10.5 day embryo"
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/note="similar to Drosophila polarity gene"
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gene


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SSWTPKNSPATRAVKLMEHEMKHVLGLTKDLFGPRIKRWVDYFPPTQSWELEI
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YFKDVESEKOLNLPKPKIPISHYPTQNDLSFPLQDIEVDAGFSNDYDLVRVAG
DMVEQISLVDFKFKPKTKGSSCFRIVYRMERTLTQAEVNEIHKQIASVDSFNVQ
IX"

BASE COUNT      2929 a 2357 c 2282 g 3046 t 158 others
ORIGIN
Query Match      2.4% Score 49; DB 14; Length 10772;
Best Local Similarity 16.9%; Pred. No. 3.55e-11;
Matches 22; Conservative 70; Mismatches 37; Indels 1; Gaps 1;

Db 1695 WYAWATTMMKMTWKMMKMTYTWMMKMYTSRTTTTTSAMMMYTWSTWKYWA 1754
Cp 1961 TTTATCTGAAATATTACAGTGTGGTTAAAGCAATATTTTACAACTTTTAAAGGTAA 1902
Db 1755 YAMMKMTWRTWARMWASARWKWTSAAAYSAWRKMKWWAYRAMKKTWMAWKWR 1814
Cp 1901 CTACTATGATATACAGGTAA-GCTACAATGGGTGTTAATTGCAAAAGTTAAGTAAGA 1843
Db 1815 WKAAWWTWRW 1824
Cp 1842 ATGTTTAA 1833

RESULT 24
LOCUS      AF012089 10772 bp DNA INV 05-AUG-1997
DEFINITION Drosophila melanogaster cysteine proteinase-1 (Cp1) gene, complete
            cds, and phenylalanyl tRNA synthetase gene, partial cds.
ACCESSION AF012089
NID        92305220

KEYWORDS
SOURCE      fruit fly.
ORGANISM    Drosophila melanogaster
            Eukaryotes; mitochondrial eukaryotes; Metazoa; Arthropoda;
            Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 4546 to 4553)
AUTHORS     Gray,Y.H., Tanaka,M.M. and Sved,J.A.
TITLE       P-element-induced recombination in Drosophila melanogaster: hybrid
            element insertion
JOURNAL     Genetics 144 (4), 1601-1610 (1996)
MEDLINE     97132596
REFERENCE   2 (bases 1 to 10772)
AUTHORS     Gray,Y.H.M., Sved,J.A., Preston,C.R. and Engels,W.R.
TITLE       Structure of the cysteine proteinase (Cp1) gene of Drosophila
            melanogaster and associated mutational effects
JOURNAL     Unpublished
REFERENCE   3 (bases 1 to 10772)
AUTHORS     Gray,Y.H.M., Sved,J.A., Preston,C.R. and Engels,W.R.
TITLE       Direct Submission
JOURNAL     Submitted (30-JUN-1997) School of Biological Sciences, University
            of Sydney, Biology A12, Sydney University, NSW 2006, Australia
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            /gene="Cp1"
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            HFRKSGVLVSLSEQLVDCSTKYNGNCGGLMDNAFRYIKDNGGIDTEKSYPEAID
            DSCHFNKGTGATDRGTDIPQDEKKAEMAVATVGPVSAIDASHESQFVSEGVN
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            4546..4553
            /gene="Cp1"
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            /gene="Cp1"
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            Join(8110..9300,9370..>9532)
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            /translation="MLTLRVQGARHLWKSTRCLASSAAPAKSPSPPOLEVSGSTYA
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            EYVRDEIDSTHPVPHQADAVRLTKDKLFERNPGLEFEETWGLADPKLILPH
            SSWTPKNSPATRAVKLMEHEMKHVLGLTKDLFGPRIKRWVDYFPPTQSWELEI
            YKONLEWFGGIMRHEILQKSGVHQSGYIAGVGLERLAWLFDIPDIRLFSWDS
            YFKDVESEKOLNLPKPKIPISHYPTQNDLSFPLQDIEVDAGFSNDYDLVRVAG
            DMVEQISLVDFKFKPKTKGSSCFRIVYRMERTLTQAEVNEIHKQIASVDSFNVQ
            IX"

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EYVRDEIDSPHYVFEHQADAVRLVTKDKLEFERNPEGLFEETWSGILADPKLILPH
SSWTKPSPATRRRAVKLEHMKHVLVGLTKDLFGPKIRYRWDTIYFFTOPSWELEI
YFKDNWLEJGCGIMRHEILQORSVGHOSIGYAFGGLERLAWILFDIPDIRLFSWSDS
GFLSOFSEKDLHNLKPKPIKSHYPCQTNLDSFLPQDIEVDAGFSPNDYDLVRSVAG
DMVEQISLVDKFKHPKTKGSSVCFRIVYRHMERLTQAEVNEIHKQIASASVDSFNVQ
IX"
BASE COUNT      2929 a  2357 c  2282 g  3046 t  158 others
ORIGIN

Query Match      2.3%; Score 46; DB 14; Length 10772;
Best Local Similarity 21.3%; Pred. No. 1.79e-09;
Matches 32; Conservative 71; Mismatches 45; Indels 2; Gaps 2;

Db 1699 AAKRKNWTWTTMKWMTWKWMMKTYRTWMMKMYTSRTTTTSAMMMYTWSTW 1748
Qy 1790 AAAGATATAAATTTTATAATTGACTTGAGTCTTAAAGCCTTGTTTAAACACATTTCTTAC 1849
Db 1749 TKYWAYAW-MKMWTRTWARMASWAWRKWKTSAAASYSNRKWW-KWAYRAMKKTW 1806
Qy 1850 TTAACCTTTGCAATTAACCATGTGACTTACCTGTAATATACATAGTACCTTTACCTT 1909
Db 1807 MWAARKWKAAMWTRWMMYTTTAAARAA 1836
Qy 1910 TAAAGTTGTAATAATATGCTTTAACCAA 1939

RESULT 25
LOCUS      AC005369      74371 bp      DNA      PRI      01-AUG-1998
DEFINITION Homo sapiens chromosome 5, BAC clone 119j3 (LBNL H175), complete
sequence.
ACCESSION      AC005369
NID      93367505
KEYWORDS      HTG.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 74371)
AUTHORS      Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
Kadner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M.,
Rojeski,H., Subramanian,S. and Martin,C.H.
TITLE      Sequencing of human chromosome 5
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 74371)
AUTHORS      Ricke,D.O.
TITLE      Large Scale Sequence Analysis and Annotation with the Sequence
Comparison Analysis (SCAN) System
JOURNAL      Unpublished
REFERENCE      3 (bases 1 to 74371)
AUTHORS      Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
Davis,C.A., Kadner,K., Miguel,T., Pitluck,S., Pollard,M.,
Rojeski,H., Subramanian,S. and Martin,C.H.
TITLE      Direct Submission
JOURNAL      Submitted (01-AUG-1998) Human Genome Center, DOE Joint Genome
Institute, Lawrence Berkeley National Laboratory, MS 74-157,
Berkeley, CA 94720, U.S.A.
COMMENT      Sequence submitted by:
DOE Joint Genome Institute.
FEATURES
source      Location/Qualifiers
1..74371
/db_xref="taxon:9606"
/map="5q"
/clone="119j3"
/chromosome="5"
/note="LBNL H175"
893..1030
/rpt_family="Alu"
2295..2438
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repeat_region      2818..2859
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/rpt_unit=GT
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/note="65% & 69% protein identity GenPept:U22377"
3431..3724
/rpt_family="Alu"
3707..3728
/note="(A)22"
/rpt_type=tandem
/rpt_unit=A
4366..4661
/rpt_family="Alu"
5327..5602
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6586..6956
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6647..6684
/note="(CA)19"
/rpt_type=tandem
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7113..7373
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complement(7830..8185)
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8258..8503
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9070..9387
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complement(9740..9845)
/rpt_family="MER42"
complement(10440..11015)
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11950..12250
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complement(12675..16977)
/rpt_family="Alu"
14175..14470
complement(14906..15259)
/standard_name="possible repeat"
15300..15613
/rpt_family="Alu"
16671..16690
/note="(T)20"
/rpt_type=tandem
/rpt_unit=T
complement(16675..16977)
/rpt_family="Alu"
complement(16993..17085)
/rpt_family="MER42"
complement(17678..18276)
/rpt_family="Alu"
19305..19583
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19814..19945
/note="(GTTT)8"
/rpt_type=tandem
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complement(19943..20222)
/rpt_family="Alu"
21202..21496
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PALLTATPPGLOPGAGGTGPGGGGACGAPRYATLEHPHCPRLVKVPSYLSKFLGLG RDCAPCEPADGDSMFFSAGEETRFARLWILLWSVCCASTFTVTIYLDWMQRFYR ERPIIFLSCYTMVSYVAFQVLQVRVVCNERFSEDGYRTVVQGTKEGCTILFMMI YFDSMASSWILSTWFLAAGMKWGEAIEANSQYFHLAAWAVPAVTRITILKMGDT IDGDLSSGVCVFLSLDRLGFVLPIWFLIFGTSFLLAGVSLFRITITLMKHGDT KTEKLERLMVRIGVESVLVTVPATIVIACYFEQAPREHWEBSWVSHOCKSLAICPA HYTPMSPCTVYMIKYLMTLVLGVTISGFWIWSGKTLHWRKFYHRLTNSRHGETTV" BASE COUNT 306 a 671 c 590 g 356 t ORIGIN									
Query Match 2.0%; Score 41; DB 21; Length 1923; Best Local Similarity 59.5%; Pred. No. 1.03e-06; Matches 175; Conservative 0; Mismatches 116; Indels 3; Gaps 2;									
Db	267	GCTGTGCACGGACATCGCCTACACACAGACCATCATGCCCAACCTCTTGGGCCACACGAA	326						
QY	399	GCTGTGCCACGGCATCGAATACAGAAACATGCGCTGCCCAACCTGCTGGGCCACGAGAC	458						
Db	327	CGAGGAGGACGAGCGCTAGAGGTGCACAGTTCTATCCCTGGTGAAGGTGAGTGCTC	386						
QY	459	CATGAAGGAGGTGCTGAGACGAGCGCGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCA	518						
Db	387	GCCGGAACCTCGCTTCTTCTGCTGCCTCATTAGCAGCACCGGTGTGCACCG-TG-CTGGA	443						
QY	519	CCCGACACCAAGAAGTCTCTGCTGCTCTGCTGCTTCCGCCCGCTGCTGCTGACCTAGA	578						
Db	444	ACAGGGCATCCCGCGTGGCGCTCTATCTGTGAGCGCGCGCGCAGGCGTCCGAAGCCCT	503						
QY	579	CGAGACCATCCGCATGCCACTCGCTCTCGTGCAGGTGAAGGACCGCTTGGCCCGGT	638						
Db	504	CATGAACAAGTTCGGTTTTTCAGTGGCCGAGCGCGTGCCTGGGAGACACTTCCC	557						
QY	639	CATGTCCGCTTCGGCTTCCCTTCCCGCCGACATGCTTGTAGTGGCAGCGTTTCCC	692						
RESULT 29									
LOCUS	128278	215 bp	DNA			PAT	30-OCT-1996		
DEFINITION	Sequence 5 from patent US 5569830.								
ACCESSION	128278								
NID	g1819054								
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unclassified.								
REFERENCE	1 (bases 1 to 215)								
AUTHORS	Bennett,A. Labavitch,J.M., Powell,A. and Stotz,H.								
TITLE	Plant inhibitors of fungal polygalacturonases and their use to control fungal disease								
JOURNAL	Patent: US 5569830-A 5 29-OCT-1996;								
FEATURES	Location/Qualifiers								
SOURCE	1..215								
BASE COUNT	15 a	8 c	25 g	26 t	141 others				
ORIGIN									
Query Match 1.9%; Score 39; DB 17; Length 215; Best Local Similarity 14.7%; Pred. No. 1.22e-05; Matches 24; Conservative 72; Mismatches 64; Indels 3; Gaps 3;									
Db	43	VCDDTTRVNDSDGHNKYSANYNGNNVGAAKTHYTH-TNVSGADSKTVDSYNAS	101						
Cp	547	CGCAGCACAGGAACCTCTTGGTGTCCGGGTGGCACTGCTTCATCACCAGCGGGATCCAAG	488						
Db	102	GTSSNGGTGDNRS-GADSVGSSKTATSNRRTKTTANNAVDSRNMGDASVSGDKNTKKH	160						
Cp	487	CGCGCGGCTCTCCAGACACTCTTCATGTCTGCTGCGCCAGCAGGTTGGCGACCGCA	428						
Db	161	AKNSADGKVGSKNGDRNNRYGTGTGKNVSNNGGKNRQVSS	203						
Cp	427	TGTTCTGGTATTCATCCCTGG-GCACAGCTGCAGGTTGGCCG	386						
RESULT 30									

LOCUS	DEFINITION	4540 bp	16-JUL-1993
RATFRZHH	Rattus norvegicus Drosophila polarity gene (frizzled) homologous mRNA, complete cds.		
ACCESSION	L02529		
NID	g310116		
KEYWORDS	frizzled gene; homologue; polarity gene.		
SOURCE	Rattus norvegicus (strain Sprague-Dawley) osteosarcoma cDNA to mRNA.		
ORGANISM	Rattus norvegicus		
REFERENCE	Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus (4540)		
AUTHORS	Chan, S.D.H., Karp, D.B., Fowlkes, M.E., Hooks, M., Bradley, M.S., Vuong, V., Bambino, T., Liu, M.Y.C., Arnaud, C.D., Strewler, G.J., and Nissenson, R.A.		
TITLE	Two homologs of the Drosophila polarity gene frizzled (fz) are widely expressed in mammalian tissues		
JOURNAL	J. Biol. Chem. 267, 25202-25207 (1992)		
MEDLINE	9309428		
FEATURES	Location/Qualifiers		
source	1. .4540		
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	/cell_type="osteoblast"		
	/tissue_type="osteosarcoma"		
	766..2691		
CDS	/note="Drosophila polarity gene (frizzled) homologue"		
	/codon_start=1		
	/db_xref="PID:g310117"		
	/translation="MAEEAVPSESRAGPSLELCAVALPGRREEVGHODTAGHRRER AHSRCWARGLLILLLEAPLLIGVRAQGVSGQQRPPPOQGGQQXNGERG ISIPDHGICQIPICDIAINQIMNELLNGEDAGLEVHQYPLVKKVQCSAE KEFLCSAPVCTVLEALPPCRSLCERAGCEALMKNKFGQWPTDLKCEKFPVHGAG ELCVGNTSDKGTPTPSLPEFTWNPQHGQGGYRGYGGAGVPGRGKFCSPRALRY PSLVNHFLEGGDCAPCEPTKVYGLMVEFPEELRSTWIGSVLLCCASTLFTVLT PLVDMRRFSYPERPIIFLSCGYTAVAVIAGFLLEDRVVCDKPAEDCAQRTVAOQTK KGCCTILFMWLYFFSMASIIWVILSLTWFLAAGKMGHEAEANSQYFHLAAWVAPA IKITLIALGVQDVGVSFCVGLNNVDALRGFVLAPFLVFIGTSLAGFVSFL RRTIMDKGTTKELEKLMVRIGVFTVPTATVIACIFYEQAFDQWERSWYAG SCKSVAIPCHLQGGVGGVPHPPMSPDFTVFMIKYLMTLIVGITSGFIWISGKTLNLS RKFYRLTNSKQETTV"		
BASE COUNT	998 a 1255 c 1220 g 1067 t		
ORIGIN			
Query Match	1.9%	Score 38;	DB 22; Length 4540;
Best Local Similarity	61.6%	Pred. No. 4.10e-05;	
Matches	181; Conservative	0; Mismatches 107;	Indels 6; Gaps 5;
Db	1116	GCTGTGCACGCATCCGTTACATCAGACCATCATGCCAACCTGCTGGGCCACAGAA	1175
QY	399	GCTGTGCCACGCATCAATACAGAACATCGCGCTGCCAACCTGCTGGGCCACGAGC	458
Db	1176	TCAGGAGACGCCGCCGCTGGAGTGCACCACTTCTACCCGCTTGGTGAAGTCAGTGCTC	1235
QY	459	CATGAAGAGAGTGTGGAGACAGCGCGCTTGGATCCCCTGGTCATGAAGCAGTGCCA	518
Db	1236	AGCCGAGCTCAAGTTCTCTCTGTCTCATATACCGGCCCTGTGTGCA-CGGT-AC-TGGA	1292
QY	519	CCCGACACCAAGAAGTCTCTGTCTCTTCGCCCCGCTCGCTCATGACCTAGA	578
Db	1293	GCAGGCGCTGCCTCTCGCGCTCCCTGTGCGAGCGCGCCAGGGCTGC--GAGGCAC--T	1349
QY	579	CGAGACCATCCAGCATCGCCATCGCTCTCGCTGCAGGTGAAGACCGCTCGCCCCGGT	638
Db	1350	CATGAACAAGTTGGCTTCCAGTGGCCACAGCTCAAGTCGCGAGAAGTTCC	1403
QY	639	CATGTCGCCCTTGGCTTCCCTCGGCCACATGCTTGAGTGCACCGCTTTCC	692

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LOCUS      AC005369      74371 bp      DNA      PRI      01-AUG-1998
DEFINITION Homo sapiens chromosome 5, BAC clone 119j3 (LBNL H175), complete
sequence.
ACCESSION  AC005369
NID         93367505
KEYWORDS   HTG.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 74371)
AUTHORS   Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
            Kader,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M.,
            Rojeski,H., Subramanian,S. and Martin,C.H.
TITLE     Sequencing of human chromosome 5
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 74371)
AUTHORS   Ricke,D.O.
TITLE     Large Scale Sequence Analysis and Annotation with the Sequence
            Comparison Analysis (SCAN) System
JOURNAL   Unpublished
REFERENCE  3 (bases 1 to 74371)
AUTHORS   Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
            Davis,C.A., Kader,K., Miguel,T., Pitluck,S., Pollard,M.,
            Rojeski,H., Subramanian,S. and Martin,C.H.
TITLE     Direct Submission
JOURNAL   Submitted (01-AUG-1998) Human Genome Center, DOE Joint Genome
            Institute, Lawrence Berkeley National Laboratory, MS 74-157,
            Berkeley, CA 94720, U.S.A.
COMMENT   Sequence submitted by:
            DOE Joint Genome Institute.
FEATURES   Location/Qualifiers
            source          1..74371
                        /organism="Homo sapiens"
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                        /note="(A)22"
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                        /rpt_unit=A
            repeat_region   4366..4661
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            repeat_region   5327..5602
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            repeat_region   6586..6956
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                        /note="(CA)19"
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001004 01 REG. 10100000, 0001 01 001000, 0001

[illegible]

[illegible]


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primer_bind 137. .161
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ORIGIN
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Query Match 1.4%; Score 28; DB 24; Length 400;
Best Local Similarity 80.4%; Pred. No. 3.33e+00;
Matches 37; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Db 255 ATATATATTTTAAAGAGTAGTGGTCTTTAGCCCTTTTAAAA 300
||||| ||||| ||| | ||||| ||||| ||||| ||||| |||||
QY 1794 ATATAATTTTATTAATGACTTGAGTACTTTAGCCCTGTTAAAA 1839

RESULT 41
LOCUS ATCOR47 1073 bp RNA PLN 02-MAR-1992
DEFINITION A.thaliana cor47 mRNA.
ACCESSION X59814
NID g16228
KEYWORDS ABA responsive gene; cold-regulated gene; cor47 gene.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryotes; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Caprales; Brassicaceae; Arabidopsis.
Thomashow, M.F.
Direct Submission
Submitted (26-MAY-1991) M.F. Thomashow, Dept. Crop & Soil Science,
Dept. of Microbiology, Michigan State University, East Lansing, MI
48824, USA
REFERENCE 2 (bases 1 to 1073)
AUTHORS Gilmour, S.J., Artus, N.N. and Thomashow, M.F.
TITLE CDNA sequence analysis and expression of two cold-regulated genes
of Arabidopsis thaliana
JOURNAL Plant Mol. Biol. 18 (1), 13-21 (1992)
MEDLINE 92119220
COMMENT cor47 product has homology with group II LEA (late embryogenesis
abundant) proteins. Lea proteins are responsive to ABA and water
stress.
FEATURES
Source Location/Qualifiers
1. .1073
/organism="Arabidopsis thaliana"
/strain="Columbia"
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/clone_lib="lambda ZAP"
/clone="PHH7.2"
1. .887
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/notes="Cold and ABA regulated gene"
/codon_start=3
/db_xref="SWISS-PROT:P31168"
/translation="NHLKATTVLKESHIFLYLLKILSRLTMAEYKNNVPEHETP
TVATESPATTTVDTRGLFDLGKKEEVKPKQETTTLESEDFHKAQISEPELAAEH
EVKENKTLLELQETDEEDENKPSVIEKLHRSNSSSSSSDEEGEERKKKKIVE
GEEDKGLVEKIEKLPKHDKTAEDDVPVSTIPVPVSVSVVYVHDHPPEERKGLVEK
IEKLPGRHDEKAEDSPATSTPLVVVTEHPVETTELPEVHEPEERKGLIEKILPG
YHAKTEEVKKEKESDD"
BASE COUNT 365 a 188 c 276 g 244 t
ORIGIN

Query Match 1.4%; Score 29; DB 19; Length 1073;
Best Local Similarity 79.6%; Pred. No. 1.17e+00;
Matches 39; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Db 1025 TCCTTTATAAAGTTGCATATGTTTACTTAAAAA 1073
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QY 1970 TCTGTATATAACTTTACATCTGTTTACCTAAAAA 2018

/organism="Mus musculus"
LOCUS A07367 1466 bp DNA PAT 18-AUG-1993
DEFINITION M.musculus VAC-alpha cdna.
ACCESSION A07367
NID 9412270
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 1466)
AUTHORS Marchese, A., Nguyen, T., Malik, P., Xu, S., Cheng, R., Xie, Z.,
Heng, H.H., George, S.R., Kolakowski, L.F. Jr. and O'Dowd, B.F.
JOURNAL Cloning genes encoding receptors related to chemoattractant
receptors
Genomics 50 (2), 281-286 (1998)
MEDLINE 98317543
REFERENCE 2 (bases 1 to 1461)
AUTHORS O'Dowd, B.F.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-1998) Department of Pharmacology, University of
Toronto, 8 Taddle Creek Rd., Toronto, ON M5S 1A8, Canada
FEATURES
Source Location/Qualifiers
1. .1461
/organism="Mus musculus"
/db_xref="taxon:10090"
1. .1461
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160. .1179
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/notes="related to chemoattractant receptors"
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/translation="MDLINSSTHVINVTSLNSTGVTPTAPKTIIAASLFMAFIIGV
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IPVLVFRTHDDHKRIKQNNYIVSTDWESKEHOTLGOVIHAACFVGRELLGLLFP
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SETEI"
BASE COUNT 390 a 365 c 274 g 432 t
ORIGIN

Query Match 1.4%; Score 28; DB 22; Length 1461;
Best Local Similarity 73.3%; Pred. No. 3.33e+00;
Matches 44; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Db 1367 ATAAATTTATATTTTAAAAATAAAGCTCTGAATCCCTAAATAAAAAA 1426
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QY 1957 ATAAACATATATCTTGTTATATAAATTTACATCCTGTTTACCTAAAAA 2016
||||| ||||| ||| ||||| ||||| ||||| ||||| |||||

RESULT 43
LOCUS A07367 1466 bp DNA PAT 18-AUG-1993
DEFINITION M.musculus VAC-alpha cdna.
ACCESSION A07367
NID 9412270
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 1466)
AUTHORS Marchese, A., Nguyen, T., Malik, P., Xu, S., Cheng, R., Xie, Z.,
Heng, H.H., George, S.R., Kolakowski, L.F. Jr. and O'Dowd, B.F.
JOURNAL Cloning genes encoding receptors related to chemoattractant
receptors
Genomics 50 (2), 281-286 (1998)
MEDLINE 98317543
REFERENCE 2 (bases 1 to 1461)
AUTHORS O'Dowd, B.F.
TITLE Direct Submission
JOURNAL Submitted (04-FEB-1998) Department of Pharmacology, University of
Toronto, 8 Taddle Creek Rd., Toronto, ON M5S 1A8, Canada
FEATURES
Source Location/Qualifiers
1. .1461
/organism="Mus musculus"
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1. .1461
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160. .1179
/gene="GPR33"
/notes="related to chemoattractant receptors"
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/product="Orphan G protein-coupled receptor"
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IPVLVFRTHDDHKRIKQNNYIVSTDWESKEHOTLGOVIHAACFVGRELLGLLFP
LWIFCYKRVATKMEKGLFKSKPKVMVAVISFFVCMVPHVHSGVLVTSQPLP
LHLLGLAVTISFNVSFVLVFTGENFKVKFKKILALFNSTFSDISSTERTQTUN
SETEI"
BASE COUNT 390 a 365 c 274 g 432 t
ORIGIN

Query Match 1.4%; Score 28; DB 22; Length 1461;
Best Local Similarity 73.3%; Pred. No. 3.33e+00;
Matches 44; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
Db 1367 ATAAATTTATATTTTAAAAATAAAGCTCTGAATCCCTAAATAAAAAA 1426
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QY 1957 ATAAACATATATCTTGTTATATAAATTTACATCCTGTTTACCTAAAAA 2016
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/codon_start=1
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/translation="MAQVLRGVTDFPFDERADAETLRKAMKGLGTDESIITLLTS
RNAORQETSAAFKTLFGRLDLDLSELTGKFKLIVALKMPSRLYDAYELKHALKG
AGTNEKVLTEIATSRPEELRAIKOVVEEYSGSLEDVVGDTSGYQRMVLYLLOAN
RPPDAGIDAEQVQDAQALFOAGELAKWGDEERFIIFGTRSVSHLRKVDKYMVTISG
FOEETIDRETSNQLLLAVVKSIRSPAYLAETLIYAMKAGGAGTDDHTFLIRVMVSR
SEIDLFNIRKFRKNFATSLYSIMIKDTSQDYKKALLLGGEDD"
BASE COUNT 423 a 291 c 327 g 425 t
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Query Match 1.48; Score 28; DB 17; Length 1466;
Best Local Similarity 80.4%; Pred. No. 3.33e+00;
Matches 37; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 1252 ATATATATTTTAAAGAGGCTAGAGTCTTTTACGCTTTTAAAA 1297
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Qy 1794 ATATAATTTTATAATGACTTGAGTACTTTAAGCCCTGTTTAAAA 1839

RESULT 44
LOCUS HUMBCI 1566 bp mRNA PRI 13-NOV-1997
DEFINITION Homo sapiens mRNA for blood coagulation inhibitor, complete cds.
ACCESSION D00172
NID 9219480
KEYWORDS blood coagulation inhibitor.
SOURCE Homo sapiens placenta cDNA to mRNA, clone_lib:lambda gtl1
clone:pk77.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1566)
AUTHORS Iwasaki,A., Suda,M., Nakao,H., Nagoya,T., Saino,Y., Arai,K.,
Mizoguchi,T., Sato,F., Yoshizaki,H., Hirata,M., Miyata,T.,
Shidara,I., Murata,M. and Maki,M.
TITLE Structure and expression of cDNA for an inhibitor of blood
coagulation isolated from human placenta: a new lipocortin-like
protein
JOURNAL J. Biochem. 102 (5), 1261-1273 (1987)
MEDLINE 88139278
COMMENT The entire amino acid sequence of the coagulation inhibitor shows
homology to those of lipocortin I, lipocortin II, and endonexin-
related proteins. The deduced amino acid sequence was
corroborated by chemical analysis of the protein.
FEATURES
Source
Location/Qualifiers
1..1566
/organism="Homo sapiens"
/note="NCBI site"
/db_xref="taxon:9606"
/clone="pk77"
/clone_lib="lambda gtl1"
/tissue_type="placenta"
136..1098
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/db_xref="PID:g219481"
/translation="MAQVLRGVTDFPFDERADAETLRKAMKGLGTDESIITLLTS
RNAORQETSAAFKTLFGRLDLDLSELTGKFKLIVALKMPSRLYDAYELKHALKG
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RPPDAGIDAEQVQDAQALFOAGELAKWGDEERFIIFGTRSVSHLRKVDKYMVTISG
FOEETIDRETSNQLLLAVVKSIRSPAYLAETLIYAMKAGGAGTDDHTFLIRVMVSR
SEIDLFNIRKFRKNFATSLYSIMIKDTSQDYKKALLLGGEDD"
polyA_signal 1545..1550
BASE COUNT 430 a 332 c 357 g 447 t
ORIGIN
Query Match 1.48; Score 28; DB 21; Length 1566;
Best Local Similarity 80.4%; Pred. No. 3.33e+00;
Matches 37; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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35..997
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/translation="MAQVLRGVTDFPFDERADAETLRKAMKGLGTDESIITLLTS
RNAORQETSAAFKTLFGRLDLDLSELTGKFKLIVALKMPSRLYDAYELKHALKG
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FOEETIDRETSNQLLLAVVKSIRSPAYLAETLIYAMKAGGAGTDDHTFLIRVMVSR
SEIDLFNIRKFRKNFATSLYSIMIKDTSQDYKKALLLGGEDD"
BASE COUNT 423 a 291 c 327 g 425 t
ORIGIN
Query Match 1.48; Score 28; DB 17; Length 1466;
Best Local Similarity 80.4%; Pred. No. 3.33e+00;
Matches 37; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 1252 ATATATATTTTAAAGAGGCTAGAGTCTTTTACGCTTTTAAAA 1297
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Qy 1794 ATATAATTTTATAATGACTTGAGTACTTTAAGCCCTGTTTAAAA 1839

RESULT 45
LOCUS E03096 1566 bp RNA PAT 26-NOV-1996
DEFINITION DNA encoding calphobindin(CPB-I).
ACCESSION E03096
NID 92171313
KEYWORDS JP 1991219875-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
Homo.
REFERENCE 1 (bases 1 to 1566)
AUTHORS Junji,N., Keishin,S., Yoshinobu,M., Fukusaburo,H., Akio,I. and
Makoto,S.
TITLE PRODUCTION OF CPB-I AND RECOMBINANT PLASMID AND TRANSFORMED YEAST
USING THEREFOR
JOURNAL Patent: JP 1991219875-A 1 27-SEP-1991;
CHEMO SERO THERAPEUT RES INST, KOWA CO
COMMENT OS Homo sapiens (human)
PN JP 1991219875-A/1
PD 27-SEP-1991
PF 25-JAN-1990 JP 1990015559
PI NAKAO JUNJI, SUGAWARA KEISHIN, MIYATSU YOSHINOBU, PI HAMADA
FUKUSABURO,
PI IWASAKI AKIO, SUDA MAKOTO
PC C12N15/12,C07K13/00,C07K13/00,C12N1/19,C12N15/81,C12P21/02, PC
(C12N1/19, C12N15/81,C12R1:645,C12R1:19),(C12P21/02, PC
C12R1:865);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FT 5'UTR 1..135
FT CDS 136..1098
FT /product="calphobindin"
FT /note="CPB-I"
FT mat_peptide 136..1095
FT /product="CPB-I"
FT 3'UTR 1099..1431.
FEATURES
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Location/Qualifiers
1..1566
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 430 a 332 c 357 g 447 t
ORIGIN
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Best Local Similarity 80.4%; Pred. No. 3.33e+00;
Matches 37; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 1252 ATATATATTTTAAAGAGGCTAGAGTCTTTTACGCTTTTAAAA 1399
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Qy 1794 ATATAATTTTATAATGACTTGAGTACTTTAAGCCCTGTTTAAAA 1839

RESULT 46
LOCUS I33410 1567 bp DNA PAT 22-JAN-1997
DEFINITION Sequence 2 from patent US 5591633.
ACCESSION I33410
NID g1824201
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

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REFERENCE 1 (bases 1 to 1567)
AUTHORS Saino,Y., Iwasaki,A. and Suda,M.
TITLE Nucleic acids encoding human placental coagulation inhibitor (PCI)
JOURNAL Patent: US 5591633-A 2 07-JAN-1997;
FEATURES Location/Qualifiers
source 1..1567
/organism="unknown"
BASE COUNT 430 a 332 c 358 g 447 t
ORIGIN
Query Match 1.4%; Score 28; DB 17; Length 1567;
Best Local Similarity 80.4%; Pred. No. 3.33e+00;
Matches 37; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Db 1353 ATATATATTTTAAAGAGCTAGAGTCTTTAGCCTTTTAAAA 1398
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Qy 1794 ATATAAATTTTATAATGACTTGACTTAAAGCCTTGTAAAA 1839
RESULT 47
LOCUS H13845 1575 bp DNA PAT 25-JAN-1994
DEFINITION H.sapiens PP4 mRNA.
ACCESSION M19384 J03264
NID g189614
KEYWORDS anticoagulant protein; thromboplastin inhibitor.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1575)
AUTHORS Grundmann,U., Abel,K.J. and Kuepper,H.
TITLE Production of the anticoagulant protein PP4 by genetic engineering
JOURNAL Patent: EP 0318703-A 6 07-JUN-1989;
BEHRINGERWERKE Aktiengesellschaft
FEATURES Location/Qualifiers
source 1..1575
/organism="Homo sapiens"
/db_xref="taxon:9606"
CDS 107..1069
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/product="PP4"
/db_xref="PID:g490122"
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RSNQRQEISAFTLFGRLDLDLSELTGKFKELIYALMKPSRLYDAYELKHALKG
AGTNEKVLTEIATSPPELRKIQVIEEYSGSLEDVVGDTSGIYQRMVLVLLQAN
RDPDAGIDEAQVEQDAQALFOAGELKWTDEKFTITGTRSVSHLRKVFQYMTISG
FQIETIDRETSGNLEQLLAVKRSIRIPAYLAETLYAMKAGTDDHTLIRVMVSR
SEIDLNRKEFRKNFATSLYSMIKGTSGDYKALLLCCGDD"
BASE COUNT 461 a 322 c 351 g 441 t
ORIGIN
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Best Local Similarity 80.4%; Pred. No. 3.33e+00;
Matches 37; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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Qy 1794 ATATAAATTTTATAATGACTTGACTTAAAGCCTTGTAAAA 1839
RESULT 48
LOCUS HUMPA84 1582 bp mRNA PRI 11-AUG-1995
DEFINITION Human placenta anticoagulant protein PP4 mRNA, complete cds.
ACCESSION M19384 J03264
NID g189614
KEYWORDS anticoagulant protein; thromboplastin inhibitor.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1582)
AUTHORS Grundmann,U., Abel,K.J., Bohn,H., Lobermann,H., Lottspeich,F. and
Kuepper,H.

TITLE Characterization of cDNA encoding human placental anticoagulant
protein (PP4): homology with the lipocortin family
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (11), 3708-3712 (1988)
MEDLINE 88234495
COMMENT Draft entry and computer-readable sequence for [1] kindly provided
by U.Grundman, 19-APR-1988.
FEATURES Location/Qualifiers
source 1..1582
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PP4-[14,20,26,48]."
/tissue_type="placenta"
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/note="PP4 mRNA"
151..1113
/codon_start=1
/product="anticoagulant protein 4"
/db_xref="PID:g189615"
/translation="MAOVLRTVTDFPGFDERADAOTLRKAMKGLGTDEESILTLT
RSNQRQEISAFTLFGRLDLDLSELTGKFKELIYALMKPSRLYDAYELKHALKG
AGTNEKVLTEIATSPPELRKIQVIEEYSGSLEDVVGDTSGIYQRMVLVLLQAN
RDPDAGIDEAQVEQDAQALFOAGELKWTDEKFTITGTRSVSHLRKVFQYMTISG
FQIETIDRETSGNLEQLLAVKRSIRIPAYLAETLYAMKAGTDDHTLIRVMVSR
SEIDLNRKEFRKNFATSLYSMIKGTSGDYKALLLCCGDD"
variation 214
/note="g in PP4-[14,26,48]; c in PP4-20"
/replace="c"
BASE COUNT 433 a 336 c 364 g 449 t
ORIGIN 82 bp upstream of SmaI site.
Query Match 1.4%; Score 28; DB 21; Length 1582;
Best Local Similarity 80.4%; Pred. No. 3.33e+00;
Matches 37; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Db 1368 ATATATATTTTAAAGAGCTAGAGTCTTTAGCCTTTTAAAA 1413
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Qy 1794 ATATAAATTTTATAATGACTTGACTTAAAGCCTTGTAAAA 1839
RESULT 49
LOCUS HUMENN 1592 bp mRNA PRI 07-NOV-1994
DEFINITION Human endonexin II mRNA, complete cds.
ACCESSION J03745
NID g182111
KEYWORDS Ca2+-dependent phospholipid binding protein; endonexin.
SOURCE Human placenta, cDNA to mRNA, (library of Clontech Laboratories
Inc.).
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1592)
AUTHORS Kaplan,R., Jave,M., Burgess,W.H., Schlaepfer,D.D. and Haigler,H.J.
TITLE Cloning and expression of cDNA for human endonexin II, a Ca2+ and
phospholipid binding protein
JOURNAL J. Biol. Chem. 263 (17), 8037-8043 (1988)
MEDLINE 88228020
COMMENT Draft entry and computer-readable sequence for [1] kindly provided
by H.T.Haigler, 06-APR-1988.
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/db_xref="PID:g182112"

/translation="MAQVLRGTVTDFFGFDERADAETLRKAMKGLGTDEESILTLTTS
RGAQKEISAFAKTLFGDLDDLKSELTKFKELIVALKMPSRLYDAVELKHALKG
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RDPDAGIDQAQALFOAGELKAGTDEERFIIFGTRSVHLRKVPDKYMTISG
FOLEETIDRETSNLEQLLAVVKSIRSIPAYLAETLIYAMKAGTDDHDLIRVMYSR
SELDLNRKFRKFNATSLYSIMIKGTSQDYKAKLLLLCGEDD"
BASE COUNT 434 a 337 c 366 g 455 t
ORIGIN 284 bp upstream of HincII site.

Query Match 1.4%; Score 28; DB 20; Length 1592;
Best Local Similarity 80.4%; Pred. No. 3.33e+00;
Matches 37; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 1378 ATATATATTTTAAAGAGGCTAGAGTCTTTAGCCTTTTAAAA 1423

QY 1794 ATATAATTTTATAATGACTTGAGTACTTTAGCCTTGTTAAAA 1839

RESULT 50 107181 1605 bp PAT 14-NOV-1994
LOCUS Sequence 12 from Patent EP 0339285.
ACCESSION 107181
NID 9589893
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1605)
AUTHORS Kaplan, R. and Jaye, M.
TITLE Recombinant endonoxin II
JOURNAL Patent: EP 0339285-A2 12 02-NOV-1989;
FEATURES Location/Qualifiers
source 1. .1605
/organism="unknown"

BASE COUNT 447 a 338 c 365 g 455 t

ORIGIN

Query Match 1.4%; Score 28; DB 17; Length 1605;
Best Local Similarity 80.4%; Pred. No. 3.33e+00;
Matches 37; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 1378 ATATATATTTTAAAGAGGCTAGAGTCTTTAGCCTTTTAAAA 1423

QY 1794 ATATAATTTTATAATGACTTGAGTACTTTAGCCTTGTTAAAA 1839

RESULT 51 HSU56813 2028 bp mRNA PRI 15-JAN-1997
LOCUS Human polycystin mRNA, partial cds.
DEFINITION U56813
ACCESSION 91477691
NID
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2028)
AUTHORS Schneider, M.C., Rodriguez, A.M., Nomura, H., Zhou, J., Morton, C.C.,
Reeders, S.T. and Weronowicz, S.
TITLE A gene similar to PKD1 maps to chromosome 4q22: a candidate gene
for PKD2
JOURNAL Genomics 38 (1), 1-4 (1996)
MEDLINE 97124839
REFERENCE 2 (bases 1 to 2028)
AUTHORS Schneider, M.C.
TITLE Direct Submission
JOURNAL Submitted (25-APR-1996) Michael C. Schneider, Renal Division,
Brigham and Women's Hospital, 75 Francis Street, Boston, MA 02115,
USA

FEATURES source 1. .2028
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/chromosome="4"

/map="4q22"
/clone_lib="Soares breast 2NbHbT"
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/note="candidate for PKD2 (autosomal polycystic kidney
disease type 2) locus"
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/product="polycystin"
/db_xref="PID:g1477692"
/translation="RNGTAWIYTSKDLNGSSHWGIATYSGAGYLDLSRTREETA
QVASLKKVMDRGTRATFDVSVNANINLFCVRLVLEPAPVATVPSWQFQPLKL
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AIGNIYRTSNVSVLLQFEDQNTFPNFEHLAYQIOFNNAAVTVFVWIKLKFIN
FNRTMSQSTMSKADLFGFAIMFFIIFLAYAQALVIFGTVQVDFSTQECIFQ
FRITGLDINFAIEEANKVLPIVFTTFVFMFILLNMLAINDTSEVKSDLAQO
KAEMELSDLRKGVHKLKLVKAKNTVDVDSISLRGGGKLNDELRLQDLKGGHTD
AETEAFTKYDQDQDELTEHEHQMDLEKEREKEDLDLHSSLPKPRMSSRSFPRLD
DSEDDDDSGHSSRRGSSISGVSIEEFQVLVRRVDRMHSIGSIVSKIDAVIVKLE
IMERAKLRREVLGRLLDGVAEERLGRDSEIRHEQMERLVRELERWESDDAASQIS
HGLGTPVLNGQPRPSRSPSSQSTEGMEGAGGSSNVHV"
966. .2028
BASE COUNT 589 a 387 c 488 g 564 t
ORIGIN

Query Match 1.4%; Score 29; DB 21; Length 2028;
Best Local Similarity 74.6%; Pred. No. 1.17e+00;
Matches 44; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Db 1962 ACTTAAATTTATTAATAACTTTACCATGGTTCATAAAAAAATAAAAAA 2020

QY 1961 ACATATATTTCTGTATATAACTTTACATCTGTTTACATAAAAAAATAAAAAA 2019

RESULT 52 MMEBK 2112 bp RNA ROD 26-APR-1996

LOCUS M.musculus mRNA for EbK receptor tyrosine kinase.

DEFINITION X81466

ACCESSION g556788

NID EbK gene; Embryo Brain Kinase.

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus

REFERENCE 1 (bases 1 to 2112)

AUTHORS Ellis, J., Liu, Q., Breitman, M., Jenkins, N.A., Gilbert, D.J.,
Copeland, N.G., Tempest, H.V., Warren, S., Muir, E., Schilling, H.,
Fletcher, F.A., Ziegler, S.F. and Rogers, J.H.

TITLE Embryo brain kinase: a novel gene of the eph/elk receptor tyrosine
kinase family

JOURNAL Mech. Dev. 52 (2-3), 319-341 (1995)

MEDLINE 96081374

REFERENCE 2 (bases 1 to 2112)

AUTHORS Rogers, J.H.

TITLE Direct Submission

JOURNAL Submitted (07-SEP-1994) J.H. Rogers, University of Cambridge, Dept.
of Physiology, Cambridge CB2 3EG, UK

REMARK revised by [3] MAT

FEATURES Location/Qualifiers

source 1. .2112
/organism="Mus musculus"
/db_xref="taxon:10090"
/tissue_type="brain"
/dev_stage="embryo"
/chromosome="4"
1. .1707
/gene="EbK"
/codon_start=1
/product="Embryo Brain Kinase"
/db_xref="PID:g556789"
/translation="FAAVSITGQAAPSOVSMKERVLSQVLSWQEPHPNGVIT
EYIKHYEKQREITYSTLKTKTSASINNLKPGTVVYFQIRAVTAAGYGNPSRLDV

ATLEASGKMEFATAVSEQNPIIAVAVAGTIIIVFMVFGTIIIGRRHCGYSKADQ
EGDELFHFEFPGTKYIDPEYEDPNRAVHQFAKELDASCIKIERVIGAGEFEVC
SGRLKPKGRVAIAIKTKLVGYTEKQRDFLCASIMGOFDHPNVHLEGVWTRGKP
VMIVIEWENGALDAFLRKHDGFTVIOVLGMLRGIAAGMYLAIDMGVYHRDLARNI
LYNSNLVCKVSDGLSRVIEDDPEAVYTTTGKIPVRWTAPEAKYRFTSASDWSY
GIVWVMSYGERPIWMSNDVLIKAIEEGRIPAPMDCPAGLHQLMDUCWKORAER
PKFOIYGLDKMIRNPSSLTGLTCSRPLSLDQSTPDFTAFCSYGEWLQIKME
RYKDNFTAAAGYNSLESVARMITDDVMSLIGITLVGHQKKIMSSIQTMRQAQLHLHGTI
QV"

polyA_signal 2045..2050
BASE COUNT 643 a 439 c 519 g 511 t
ORIGIN

Query Match 1.4%; Score 29; DB 22; Length 2112;
Best Local Similarity 69.3%; Pred. No. 1.17e+00;
Matches 52; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Db 2034 TATATTTCATAAATAATCATGCTTATTGTTAAATCAATCAATATTTTCTTAA 2093

Qy 1945 TAAATATTTCAGATAACATTATTTCTGTATATAAATTTTACATCTCTGTTTACCTAA 2004

Db 2094 AAAAAAAAAAAAAA 2108

Qy 2005 AAAAAAAAAAAAAA 2019

RESULT 53
LOCUS MMU43320 2260 bp mRNA ROD 24-FEB-1996
DEFINITION Mus musculus putative transmembrane receptor (frizzled 7) mRNA,
complete cds.
ACCESSION U43320
NID g1151257

KEYWORDS house mouse.
SOURCE Mus musculus.
ORGANISM Mus musculus.
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.

REFERENCE 1 (bases 1 to 2260)
AUTHORS Wang,Y., Macke,J.P., Abella,B.S., Andreasson,K., Worley,P.,
Gilbert,D.J., Copeland,N.G., Jenkins,N.A. and Nathans,J.
TITLE A large family of putative transmembrane receptors homologous to
the product of the Drosophila tissue polarity gene frizzled
JOURNAL J. Biol. Chem. 271 (8), 4468-4476 (1996)

MEDLINE 96224032
REFERENCE 2 (bases 1 to 2260)
AUTHORS Abella,B., Wang,Y., Macke,J.P. and Nathans,J.
TITLE Direct Submission
SUBMITTED (14-DEC-1995) Jeremy Nathans, Molecular Biology and
Genetics, Johns Hopkins Medical School, 725 N. Wolfe Street,
Baltimore, MD 21205

FEATURES
source Location/Qualifiers
1..2260
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="2"
/map="2q33-34"
362..2080
/gene="frizzled 7"
362..2080
/gene="frizzled 7"
/note="putative transmembrane receptor"
/codon_start=1
/product="transmembrane receptor"
/db_xref="PID:g1151258"

/translation="MRGCGTAAASHPLGLCALVLALLCALPTDTRAPQYHGEKGISVP
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SGMYAPVCTVLDQAIPCRSLCARQCEALMNKFGQFWRLECRNFVPHGAEIC
VGNSTDSGGAGSGSTAYTAPYLPDPPTAMSPSDGRSLSPFSCPRQLKVPYVL
GYRFLGDCRCPAFCGRCAGLMYKFEERFARLWVMSVLSCASTLFTLVLYLVD
MRFSYFPIPLFSLGCVFMVAHVAGFLELDRAVCVERSDSDGYRTVAQGTKEGC
TILFWLYLFTGMASISIMWVILSLTWFLAAGKWKHGAIEANSQYFLAANAVPAVKTI
TILAMQVDDGLLSGVCIVGLSSVDALRGFVLAPLFLVILFTIGTSLFLLAGFVSLFRIT

IMKHDTGTEKLEKLMVRIGVSVLYTVPATIVLACYFEQAFAHREHWERTWLLQTKS
YAVPCPPPHFSPMSPDFTFVMIKYLMTMIVGTTTGTWISGKTLQSWRRFYHRLSHSS
KGETAV"

BASE COUNT 362 a 739 c 677 g 481 t 1 others
ORIGIN

Query Match 1.4%; Score 29; DB 22; Length 2260;
Best Local Similarity 59.3%; Pred. No. 1.17e+00;
Matches 140; Conservative 0; Mismatches 93; Indels 3; Gaps 2;

Db 560 CTGCCCAACCTGCTGGGCCACACGAACGAAGAGGCGGGGCTCGAGTGCCACCATTC 619

Qy 433 CTGCCCAACCTGCTGGGCCACGAGACCATGAAGGAGGTGCTGGAGCAGCGCGCTTGG 492

Db 620 TACCTCTGGTAAAGTGCAGTGTCTCTGAGCTACGCTTCTTCTTATGCTCTATGTAC 679

Qy 493 ATCCCGCTGGTCAATGAAGCAGTGCACCGGACACCAAGAAGTTCTGCTGCTCTTC 552

Db 680 GCACCCGTGTGCACCG-TG--CTCGACCAAGCATTCCTCGTCCGTTCTCTTGTGCGGAG 736

Qy 553 GCCCGGTGCTGCTGATGACCTAGACGACCATCCACCATGCCACTGCTCTGCGTG 612

Db 737 CGCGCCGACAGGGTGCAGAGCGCTCATGAACAGTTTCGGCTTCAGTGGCCAGA 792

Qy 613 CAGGTGAAGGACCGCTGCGCCCGGTGTCATGTCGGCTTCGCCCTCCCTCGGCCGA 668

RESULT 54

LOCUS PFSC04076 4798 bp DNA INV 08-DEC-1997

DEFINITION Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from

contig 4-76, complete sequence.

ACCESSION AL010253

NID 92673812

KEYWORDS HTG.

SOURCE malaria parasite.

ORGANISM Plasmodium falciparum

REFERENCE 1 (bases 1 to 4798)

AUTHORS Lawson,D.

TITLE Direct Submission

JOURNAL Submitted (06-DEC-1997) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge

CB10 1SA, UK

COMMENT IMPORTANT: This sequence is unfinished and does not necessarily

represent the correct sequence. Work on the sequence is in progress

and the release of this data is based on the understanding that the

sequence may change as work continues. The sequence may be

contaminated with foreign sequence from E.coli, yeast, vector,

phage etc.

For more information about this sequence or the Malaria Project,

see http://www.sanger.ac.uk/Projects/P_falciparum.

FEATURES
source Location/Qualifiers
1..4798
/organism="Plasmodium falciparum"
/db_xref="taxon:5833"
/chromosome="4"
/clone="4-76"

BASE COUNT 1785 a 483 c 459 g 2071 t

ORIGIN

Query Match 1.4%; Score 29; DB 14; Length 4798;

Best Local Similarity 75.4%; Pred. No. 1.17e+00;

Matches 43; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Db 466 TTTTCTTTTCTTTTTCAGATAACGGATTATTAGATGATATATAAATATAT 522

Cp 2019 TTTTCTTTTCTTTTTCAGATAACGGATTATTAGATGATATATAAATATAT 1963

RESULT 55

LOCUS PFSC04015 7964 bp DNA INV 27-JUN-1998

DEFINITION Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from

contig 4-15, complete sequence.

gene	PAAPSNPEPMDEDDDDIPF" complement(5739.. .6089) /gene="y7cB" CDS complement(5739.. .6089) /gene="y7cB" /note="f116; 100 pct identical amino acid sequence and equal length to yJCB_ECOLI SW: P32700" /codon_start=1 /transl_table=11 /label=b4060 /product="hypothetical 13.0 kD protein in ssb-soxs intergenic region" /db_xref="PID:g1790495" /translation="MTHASREQRAVGIGSFQRCMLATLTGGVLLRWQLLSAVMM FLASTLINIRFRSDYVGLAVISSGLGVVSACWFAMGLLGITMADITAIWHNIESVMIE ENNQTPQWPMILT" 6450.. .8036 /gene="y7cC" CDS 6450.. .8036 /gene="y7cC" /note="o528; 100 pct identical to yJCC_ECOLI SW: P32701; similar to Azorhizobium caulinodans hypoth. protein, ntrC 3' region" /codon_start=1 /transl_table=11 /label=b4061 /product="hypothetical 60.8 kD protein in ssb-soxs intergenic region" /db_xref="PID:g1790496" /translation="MSHRARHQLALPGLIFLVLPILISLWIAFLWAKSEVNNQRLRT FAQLADKSELVIRQADLVSDAAERYQGQCTPAHQKRMUNIRGLYILNELIYARDN HFUCSSLIAPVNGYTIAPADYKREPNNVSIYYIDPFFSGKMYQWQNGYVAVINPL FWEVMSDDPTLQWGYDVTIKTFSSLSKEASAATESPLIHLKDLTWQRNGYIATVY STKRPAIATVATSYQRLITHFYNHLIFALPAGILGSLVLLWLRLRONYLSPKRLQ RALEKQCLCYOPIIDIKTEKICIGAEALLRWPEGQGLIMNPAEFIPLAKEGMEIQI TDYIVNFRDLGDIATHADRYVINSLSRDPHTSRLRLANQKTEQVAVRQQKIF EVTEHAPLDVDMKMPIILAFARAGIEVAIDDFGIGYSLNHLNLSLNDILKIDKSEVE LTTHTKSHLIAEHIIELAHSLGLKTAIEGVETEQQVNMRLKRGVRYCOGWEFFAKAMP PQVFMQMEQLPALELTRGQ" complement(8039.. .8362) /gene="soxS" CDS complement(8039.. .8362) /gene="soxS"	gene	complement(5460.. .5645) /gene="F28J12.20" /number=1 5460.. .7702 /gene="F28J12.20" complement(5646.. .5969) /gene="F28J12.20" /number=1 complement(5970.. .6074) /gene="F28J12.20" /number=2 complement(6075.. .6164) /gene="F28J12.20" /number=2 complement(6165.. .6265) /gene="F28J12.20"	gene	complement(5460.. .5645) /gene="F28J12.20" /number=1 5460.. .7702 /gene="F28J12.20" complement(5646.. .5969) /gene="F28J12.20" /number=1 complement(5970.. .6074) /gene="F28J12.20" /number=2 complement(6075.. .6164) /gene="F28J12.20" /number=2 complement(6165.. 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complement(5646.. .5969) /gene="F28J12.20" /number=1 complement(5970.. .6074) /gene="F28J12.20" /number=2 complement(6075.. .6164) /gene="F28J12.20" /number=2 complement(6165.. .6265) /gene="F28J12.20"	gene	complement(5460.. .5645) /gene="F28J12.20" /number=1 5460.. .7702 /gene="F28J12.20" complement(5646.. .5969) /gene="F28J12.20" /number=1 complement(5970.. .6074) /gene="F28J12.20" /number=2 complement(6075.. .6164) /gene="F28J12.20" /number=2 complement(6165.. .6265) /gene="F28J12.20"	gene	complement(5460.. .5645) /gene="F28J12.20" /number=1 5460.. .7702 /gene="F28J12.20" complement(5646.. .5969) /gene="F28J12.20" /number=1 complement(5970.. .6074) /gene="F28J12.20" /number=2 complement(6075.. .6164) /gene="F28J12.20" /number=2 complement(6165.. .6265) /gene="F28J12.20"	gene	complement(5460.. .5645) /gene="F28J12.20" /number=1 5460.. .7702 /gene="F28J12.20" complement(5646.. .5969) /gene="F28J12.20" /number=1 complement(5970.. .6074) /gene="F28J12.20" /number=2 complement(6075.. .6164) /gene="F28J12.20" /number=2 complement(6165.. .6265) /gene="F28J12.20"	gene	complement(5460.. .5645) /gene="F28J12.20" /number=1 5460.. .7702 /gene="F28J12.20" complement(5646.. .5969) /gene="F28J12.20" /number=1 complement(5970.. .6074) /gene="F28J12.20" /number=2 complement(6075.. .6164) /gene="F28J12.20" /number=2 complement(6165.. .6265) /gene="F28J12.20"	gene	complement(5460.. .5645) /gene="F28J12.20" /number=1 5460.. .7702 /gene="F28J12.20" complement(5646.. .5969) /gene="F28J12.20" /number=1 complement(5970.. .6074) /gene="F28J12.20" /number=2 complement(6075.. .6164) /gene="F28J12.20" /number=2 complement(6165.. .6265) /gene="F28J12.20"	gene	complement(5460.. .5645) /gene="F28J12.20" /number=1 5460.. .7702 /gene="F28J12.20" complement(5646.. .5969) /gene="F28J12.20" /number=1 complement(5970.. .6074) /gene="F28J12.20" /number=2 complement(6075.. .6164) /gene="F28J12.20" /number=2 complement(6165.. .6265) /gene="F28J12.20"	gene	complement(5460.. .5645) /gene="F28J12.20" 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JOURNAL REFERENCE	Unpublished (1998) 2 (bases 1 to 115641) Theologis,A.	gene	QAMRDGANVKGIFYVWSLNDNFEMWLEFGYKVRFGLFHVDLTTLTKRSQKQASWYKNKIE EHNRRDIVDN" 11528. .15385
JOURNAL AUTHORS	Direct Submission Submitted (11-MAR-1998) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA	CDS	/gene="F8K4.3" join(11528. .11625,12458. .12539,12625. .12694,13043. .13103. 13216. .13291,13473. .13547,13658. .13745,13819. .14071. 14162. .14277,14372. .14630,14741. .14843,14938. .15046, 15190. .15385)
JOURNAL REFERENCE	3 (bases 1 to 115641) Theologis,A.		/gene="F8K4.3"
JOURNAL AUTHORS	Direct Submission Submitted (01-JUL-1998) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA		/note="Similar to F411.26 putative beta-glucosidase gi 3128187 from A. thaliana BAC gb AC004521. ESTs gb IN97083, gb F19868 and gb F15482 come from this gene."
JOURNAL TITLE	4 (bases 1 to 115641) Theologis.		/codon_start=1 /evidence=not_experimental /db_xref="PID:g3367517"
JOURNAL REFERENCE	Direct Submission Submitted (01-AUG-1998) Plant Gene Expression Center, 800 Buchanan St., Albany, CA 94710, USA		/translation="MSPTISSAAATPTPSNGSTFSAALALLVRNSCLHQTSDQSE PPSDELFGTASSAFOYEGAFITDGGKLNWDVFAHENGKIVDNGSGDIATQOYHRY MEDIQSMNFGVNSYRSLISWSRVNPGRGVINYKGIKYNILDALIKLITPPTV LNHFDPPELENKRFKSWLSEMOKDFGLADICFKHFGDRVKWITINENQHSILAY RSLGFLPPARCSPYGNCTHGNSTEFIAAHNMILAHAKAIQIYRTKYQREQGIIGI VNTSWFEPISDIAADNAERAQSFYSWILDPVYGYPEMWLLGKALPKFSNN ENMSYKSDDELGINHYTSYFIQDCLITACNSDGDGKSEGALALDRKGNVSGEL TDVNWQHDIPNGFRKMLNKNRYHNIPYITENGFGQLOKQPETTVEELLHDKRKQY LSGYLDALKAARDGANVKGIFYVWSLNDNFEMWLEFGYKVRFGLFHVDLTTLTKRPKQSA TWYKNFQENQVNIQDIDK"
JOURNAL AUTHORS	5 (bases 1 to 115641) Theologis.	gene	/evidence="F8K4.4" 16933. .18807
JOURNAL TITLE	Direct Submission Submitted (04-AUG-1998) Plant Gene Expression Center, 800 Buchanan St., Albany, CA 94710, USA	CDS	/gene="F8K4.4" join(16933. .17047,17094. .17705,17750. .18807) /note="Strong similarity to unknown protein T28M21.21 gi 2088661 from A. thaliana BAC gb AF002109."
COMMENT	This sequence is of BAC F8K4 from Arabidopsis thaliana chromosome 1. The sequence does not represent the sequence of the entire insert of this clone. It is shorter by 3062 bp because we submit only the unique sequence of the clone. In order to facilitate the joining of overlapping clones in the future for creation of larger contigs, we provide a small overlap (200 bp) between overlapping submitted clones. The 3' end of this sequence overlaps by 200 bp the 5' end of the sequence of BAC F19K23. Location/Qualifiers 1. .115641 /organism="Arabidopsis thaliana" /cultivar="Columbia" /db_xref="taxon:3702" /chromosome="1" /clone="F8K4" 1468. .3346 /gene="F8K4.1" join(1468. .1959,2350. .2575,2668. .2890,3055. .3346) /gene="F8K4.1" /note="Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb AF020814 from Pisum sativum." /codon_start=1 /evidence=not_experimental /db_xref="PID:g3367515"		
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JOURNAL AUTHORS	/note="Similar to beta-glucosidase BCQ60 precursor gb 41869 from Hordeum vulgare." /codon_start=1 /evidence=not_experimental /db_xref="PID:g3367516"	gene	/evidence=not_experimental /db_xref="PID:g3367532"
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36009. .36170.36301. .36502.36594. .36730.36877. .37015, 37164. .37370.37463. .37943.38040. .38256.38354. .38443, 38687. .39166) /gene="F8K4.6" /note="Contains similarity to gb U51898 Ca2+-independent phospholipase A2 from Rattus norvegicus." /codon_start=1 /evidence=not_experimental /db_xref="PID:g3367519" /translation="MSSCTSSPSAVDEPDLGFRIDLDWTAGDSEDQVALRLLESQLMVA LPADHTVYVGLKGGIDEGGLENVLEMRVKKREPLRAVTLMAKVGSGQYDGVG VLTLMRSDMPAAIPAPADIVASSCGVHWKVTLSLSGCGLLVMPVEVTEPLPLEK LCLEHNKLSVLPKGLKLNKILRVNDNNMLISVPELRQCVGLVLEHNKLVRLPL LDPSLGRANTSVFSGASRHKLSAFSLPIRSSSCHPLASTLVKIMQDEGRSVI KDENAVQLLSMITSQNVQVACVALSDVDVGMQLMKCDIMKPTETVLKSS SPENVGLVTVTFVAFVSDVSQKMLTKMLKALKSCAHKNPEVQOALLAVGNLA FCLENRLITSESRELLMLRVTPPEPRVKAARALAILGENILRRSIKGRVPK QGLRTLWDGGMKGLATVOILKEJKSGKPIHEFLDLIGTSTGGMALALGVKLM TLEOCEEYKKNLGLVFAESVPKONEASWREKLDQLYKSSQSQRVVIHSGKHSANE FERLLKCADEDGLLIESAVKNVPKVFVSTLVSPVPAQFFIFRNYOYVPGTPEMS YAFSDHSGSTLSTSDAQGYKQSAFMSGCKHOVQWQAIASSAAPYYLDLDFSVGT NSYRWQDGAIVANNPTIFAIREAQLLPDTKIDCLVSGSGVPTVRKGGWRYLDTG QVLTESACSVERVEALSTLLPMLPEIOYFRFNPVDDRCGMELDETDAIWLKEAAI EEFIQSNPOVKNCYCERITLPELDEKWCNDLKPFEMNGKLPNSRVESSPSLGWRNV LLMEAQHSQDSGRVKYHARALESGSCNNGIKLSLHTTATPGCCQKPSGTAFFPFTS PLITGSLPSPLLTFPELPGQKFNRIWVPLSLDGGHGVKTVSPSPSPRQROLYL PLRMHEKQLNPQVQILHLSDNDSNGILSQWNVFAEPPGLADKFLQSKVSI LSVMQSNRRKASLNSICISDLVRKCKFCQGNIIHRYIGRQTLVMDQEDQIASEFM FRRTVPSAHLPTDDIRMMVGAWRDRIIVFSGTFGPTQAVRAFLDSGAKAVIGPSNEP QETPLITSQGSSEYNIGDQKFEIEEEDVEEVEETEEEMEPPTPTSDWEDSDH EKTNRDGYCYGLWEDDEVEFVQCLYDQLFERNRSVDVALOKALASHRLRYTCHL PNV" complement(40020. .41560) /gene="F8K4.7" complement(join(40020. .40765,40848. .41037,41130. .41311, 41311, Note: remainder of annotations omitted. Query Match 1.4%; Score 29; DB 19; Length 115641; Best Local Similarity 73.8%; Pred. No. 1.17e+00; Matches 45; Conservative 0; Mismatches 16; Indels 0; Gaps 0; Db 16446 TTTTITTTTTTTTTTTGGTAAAAAATTCGAGTTGTATACAAAAATAATATT 16505 Cp 2019 TTTTITTTTTTTTTTTAGGTAACAGATGTAAGTTTATATACAGATATATGTT 1960 Db 16506 T 16506 Cp 1959 T 1959 RESULT 60 LOCUS ECOUW89 176195 bp DNA BCT 17-DEC-1993 DEFINITION E. coli chromosomal region from 89.2 to 92.8 minutes. ACCESSION U00006 NID 9409785 KEYWORDS SOURCE Escherichia coli (sub_strain MG1655, strain K-12) (library: lambda) DNA. ORGANISM Escherichia coli Eubacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia. REFERENCE 1 (bases 1 to 176195) AUTHORS Blattner,F.R., Burland,V., Plunkett,G. III., Sofia,H.J. and Daniels,D.L. TITLE Analysis of the Escherichia coli genome. IV. DNA sequence of the region from 89.2 to 92.8 minutes Nucleic Acids Res. 21 (23), 5408-5417 (1993) 94089392 REFERENCE 2 (bases 1 to 176195) AUTHORS Blattner,F.R. TITLE Direct Submission JOURNAL Submitted (03-SEP-1993) 608-263-7459	This sequence was determined as part of the E. coli Genome Project (Frederick R. Blattner, director) at the University of Wisconsin-Madison. Supported by award HG00301 from the NIH Human Genome Project. The entire sequence was independently determined from E. coli MG1655; overlaps and conflicts with other sequence determinations are annotated. The start of this entry overlaps the end of the entry ECOUW87 (L19201) by 93 bp. NOTE: An update was submitted on 25-OCT-1993, reflecting a correction to the heme sequence. Location/Qualifiers 1. .176195 /organism="Escherichia coli" /strain="K-12" /sub_strain="MG1655" /notes="This sequence comprises the following lambda clones: EC18-126, EC14-54, EC21-52, EC17-24, EC17-203, EC19-105, EC18-208, EC18-110, EC17-200, EC18-33, EC30-262, EC30-41, EC30K637-2a, EC30K637-5, EC27-975, EC22-27; M13mp19 or Janus vectors were used for subcloning" /db_xref="taxon:562" 1. .1257 /gene="katG" /note="corresponds to M21516; ECOKATGA(1225. .2805)" 1. .1737 /gene="katG" /standard_name="catalase HPI; catalase-peroxidase; catalase" /EC_number="1.11.1.6" /note="CG Site No. 14983" /codon_start=1 /transl_table=11 /product="catalase hydroperoxidase I" /db_xref="PID:g396289" /translation="AITSGLVWVQTPTQNSYFFENLFKVEYVQTRSPAGAIOFEA VDAPILIPDPSPKRRKPTMLVDTLIRFOPEFKISIRPLNDPQAFNEARXWFK LTHRDMPKRSYIGEVPEKEDLIWQDPLQPIYNTEQDIIDKFAIDSGLSVSELV SWASASTFRGGDRGGANGARLALMPORDMDVNAARALPVEIKIQESGKASLV DIIVLAGVYGEKAAAGLSIHVPFAPFARDARQDQTDIEMFELLEPTADGFRNRA RIVDTESLITDKAQQLTAPETALVGGMRVILGANFDGSKNGVFTDRVGLSNDF FVNLDDMYEWKATDESKLEFEGRDRETGEVKFTASRADLVFGSNVSLRAVEAVASS DAHEKFVDFVAAVKVVNLDREFLL" 1. .93 /gene="katG" /note="93 bp overlap with end of L19201 (ECOWU87)" 1. .161 /gene="katG" /note="corresponds to lambda clone EC18-126" 156. .15760 /note="corresponds to lambda clone EC14-54" misc_difference 938 /gene="katG" /note="G in M21516; C here" 1266. .1305 /note="putative" 1317. .2255 /note="similar to Desulfohalobus ambivalens hypoth. 28.3 kDa protein in sor 3' region" /codon_start=1 /transl_table=11 /label="ORF_0312" /db_xref="PID:g409786" /translation="MGERKLHTGSLMSAAGSNPLAISGLVVLTLIWSYSWIFMKQVT SYGAFDFTALRCIFGALVFLVILLRGRMRPTPKVTALAIQTCCGMVGLAOWAL VSGAGKVAILSYTYPFWVIFAAFLGERLPRGOYFALLIAFGLEFLQWQLDPS SKMSNMLALLSGVSGASAIYAKRIYARHPRVDLSLTSWQMLYALVMSVVALLPQ REIDWQPTFWALAYSAILATALAWSLWFLVNLKPLPASLSTLSTLAVPVCGLFSLWML LGENPGAVEGSGIVLILALALVSRKKKEAVSKRI" 1429. .1432 /note="TTT in M21516; TTTT here" misc_difference 1720 /note="C in M21516; G here" complement(2282. .2899) /codon_start=1	COMMENT	FEATURES	Source
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2912..3053
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element"
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NNVIYDKIVAPARLALGAQGDALATWFEACRSRGATTMAGCKTQALALAEI
CTILLEGEERKAMLAEOHVPTPALEREIANTYLSGVFGESGLAAAHVINGLTAI
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/notes="corresponds to lambda clone EC21-52"
7578..7699
terminator
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7771..7800
promoter
/notes="promoter matrix score of 48; putative; within ORF
o359, which would suggest alternate start codon"
7771..8850
CDS
/notes="similar to phosphotransferase system enzyme II"
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LINSLTQWLQGMQGSIVMLAVIMGLMLAFDGMGPVKNVAYAFMLICVAGOGVYTVVAI
AAYGICPPLIGMLATLIGRKNFSAEERETGKAAALVMGCVGVTEGAIPFAAADPLRVI
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CDS
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Note: remainder of annotations omitted.

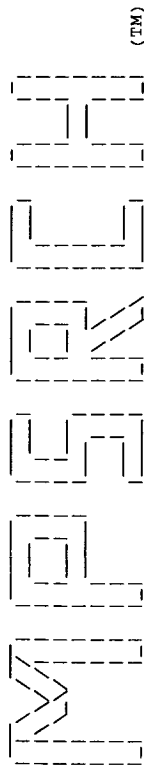
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Best Local Similarity 71.9%; Pred. No. 3.33e+00;
Matches 46; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Db 137388 CCTTCTCGCACCACTTCACCGCCGTGAACACCTCGCCGCCCAATGTCGATCACATGG 137447
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Cp 1090 CCTTCTCGCACCGCTTCACCGAGGTGATCACCAGCTCCACCACCTGTTCTTGTCCCATGA 1031

Db 137448 TCAG 137451
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Cp 1030 CCAG 1027

Search completed: Thu Nov 5 10:57:29 1998
Job time : 6226 secs.

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(TM)

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Thu Nov 5 12:14:45 1998; MasPar time 291.26 Seconds
Tabular output not generated. 946.855 Million cell updates/sec

Title: >US-08-848-439-1
Description: (1-2027) from US08848439.seq
Perfect Score: 2027
N.A. Sequence: 1 GRATTCGGCTTCATGCGCT.....AAAAAAGGCGGCGGCGC 2027
Comp: CTTAAGCCGGAAGTACCGGA.....TTTTTTTTTTCGCGGCGG

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 188442 seqs, 68026449 bases x 2

Post-processing: Minimum Match 0%
Listing first 60 summaries

Database: n-genesq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40

Statistics: Mean 9.846; Variance 6.883; scale 1.431

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	ID	Description	Pred. No.
1	201	9.9	204	20	Human gene signature	1.01e-97
2	58	2.9	2334	37	Human frizzled gene 5	6.84e-16
3	56	2.8	2421	37	Mouse frizzled gene 8	7.60e-15
4	44	2.2	91	9	Oligonucleotide probe	9.73e-09
5	45	2.2	172	32	Human interleukin 8 a	3.11e-09
6	43	2.1	204	1	Base substituted E.co	3.03e-08
7	41	2.0	91	9	Oligonucleotide probe	2.88e-07
8	40	2.0	100	32	Human IL4 receptor an	8.76e-07
9	40	2.0	114	12	Generic DNA sequence	8.76e-07
10	40	2.0	114	12	Generic DNA sequence	8.76e-07
11	40	2.0	204	1	Base substituted E.co	8.76e-07
12	39	1.9	114	12	Generic DNA sequence	2.85e-06
13	38	1.9	114	12	Generic DNA sequence	7.95e-06

ALIGNMENTS

RESULT 1

ID	T23535	standard; cDNA to mRNA; 204 BP.
AC	T23535;	
DT	02-SEP-1996	(first entry)
DE	Human gene signature HUMG05382.	
KW	Gene signature; messenger RNA; mRNA; relative abundance; frequency;	
KW	human; cloning; mapping; non-biased library; diagnosis; detection;	
KW	cell typing; abnormal cell function; ss.	
OS	Homo sapiens.	
PN	WO9514772-A1.	
PD	01-JUN-1995.	
PF	11-NOV-1994; J01916.	
PR	12-NOV-1993; JP-355504.	
PA	(NATS/) MATSUBARA K.	
PA	(OKUB/) OKUBO K.	
PI	Matsubara K, Okubo K;	
DR	WPI: 95-206931/27.	
PT	Identifying gene signatures in 3'-directed human cDNA library - e.g.	
PT	for diagnosis of abnormal cell function, by preparing cDNA that	
PT	reflects relative abundance of corresp. mRNA in specific human	
PT	tissues	
PS	Claim 1; Page 1393; 2245pp; Japanese.	

CC A single-stranded DNA (or its complementary strand or the corresp.
 CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
 CC given in T19001-T26837 and which is able to hybridise to part of
 CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
 CC sequences were obtained from 3'-directed cDNA libraries prepared
 CC from various human tissues; synthesis of cDNA was initiated from the
 CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
 CC untranslated sequence is unique to a particular mRNA species, almost
 CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
 CC is constructed so as to reflect accurately the relative abundance of
 CC different mRNAs in the particular tissue from which it was derived.
 CC The appearance frequency of a given GS in a cDNA library can be
 CC determined (esp. using primers and probes derived from the GS
 CC sequences) as a means of diagnosing abnormal cell function or for
 CC recognising different cell types.
 SQ Sequence 204 BP; 54 A; 59 C; 35 G; 55 T;

Query Match 9.9%; Score 201; DB 20; Length 204;
 Best Local Similarity 99.5%; Pred. No. 1.01e-97;
 Matches 201; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 gatctcagctccgttccccaagacactctctagctgtctccagttctcagctggcagct 60
 Qy 1207 GATCTCAGCTCCGTTCCCAAGCACACTCTCTAGCTGTCTCCAGTCTCAGCTGGGAGCT 1266
 Db 61 tccccctgcttttcacagctttgcattcccccagcatttctcagttataaggccagag 120
 Qy 1267 TCCCCCTGCTTTTCACAGTTTGATCCCAAGTCTCTGAGTTATAGGCCAGGAG 1326
 Db 121 tggatagctgttttcacctaagagaaagccacccagcgaattctgtagaataattcaact 180
 Qy 1327 TGGATAGCTGTTTTCACCTAAGGAAAGCCACCCGGAATCTGTAGAAATATTCAACT 1386
 Db 181 antaaatcatgaatttttta 202
 Qy 1387 AATAAATCATGAATTTT 1408

RESULT 2
 ID T89889 standard; DNA; 2334 BP.
 AC T89889;
 DT 27-APR-1998 (first entry)
 DE Human frizzled gene 5 (Hfz5) encoding a Wnt receptor.
 KW Wnt receptor; human frizzled gene 5; Hfz5 gene;
 KW signal transduction; cancer; cell growth; cell proliferation;
 KW mammary tumour; oncogene; therapy; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 321..2078
 FT /*tag= a
 PN WO9739357-A1.
 PD 23-OCT-1997.
 PF 11-APR-1997; U06049.
 PR 12-APR-1996; US-015307.
 PA (UJJO) UNIV JOHNS HOPKINS.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J,
 PI Nusse R, Samos CH, Wangy;
 DR WPI; 97-526631/48.
 DR P-PSDB; W31271.
 PT Identification of Wnt receptor binding modulators - useful for
 PT treatment of cancer and growth, development or proliferation related
 PT disorders
 PS Disclosure; Page 36-37; 61pp; English.
 CC This sequence comprises novel human frizzled gene 5 (Hfz5)
 CC that encodes a transmembrane receptor, frizzled-5 (see w31771), a
 CC Wnt receptor (WntR). Novel frizzled family members have been
 CC identified in Drosophila, mouse, human and Caenorhabditis (see
 CC T89888-92) and are considered to be Wnt receptors. Wnt receptors
 CC which modulate the binding of a Wnt polypeptide (secreted proteins
 CC can be used in a novel, claimed method of screening for compounds
 CC involved in cell-to-cell signalling) to a Wnt receptor. Wnt is
 CC involved in (mammary) cancer and other processes involving growth,

CC development and proliferation (both normal and abnormal).
 CC Modulators identified by the claimed method are useful for
 CC treatment of diseases related to these conditions.
 SQ Sequence 2334 BP; 356 A; 803 C; 736 G; 439 T;
 Query Match 2.9%; Score 58; DB 37; Length 2334;
 Best Local Similarity 59.9%; Pred. No. 6.84e-16;
 Matches 175; Conservative 0; Mismatches 117; Indels 0; Gaps 0;
 Db 439 tctgcccggcctcgctacacacctgaagcaccatgccccaccagttcaaccacgacacgc 498
 Qy 401 TGTGCCAGCGGCATCGATACCAACATCGCGCTGCCCAACCTGCTGGGCCAGGACCA 460
 Db 499 aggacgagcgccgctgaggtgcaccagttcttgcgcgtgtgagatccaatgctgc 558
 Qy 461 TGAAGAGGTGCTGGAGCAGCGCGGCTGGATCCCGCTCATGAAGCAGTGCAC 520
 Db 559 cggacctgcgcttctctctatgcactatgtacacgcccactgtctgcccagctaccaca 618
 Qy 521 CGGACACCAAGAAGTTCCTGTCTGCTCTTCCGCCCGCTGCTCGATGACCTAGACG 580
 Db 619 agccgctgcccctgcgcgtcggtgtgcgagcgccgaagccggctgctgcgcgctga 678
 Qy 581 AGACCATCCAGCATGCCACTGCTCTGCTGCGAGTGAAGGACCGCTCGGCCCGGTCA 640
 Db 679 tgcgcagtaagcttcgcctgcccgcgagcgcatgagctgcacgcctccc 730
 Qy 641 TGTCCGCTTCCGCTTCCCGCTGCCCGGACATCTTGTAGTGCAGCGCTTTTCCC 692

RESULT 3
 ID T89892 standard; DNA; 2421 BP.
 AC T89892;
 DT 27-APR-1998 (first entry)
 DE Mouse frizzled gene 8 (Mfz8) encoding a Wnt receptor.
 KW Wnt receptor; mouse frizzled gene 8; Mfz8 gene;
 KW signal transduction; cancer; cell growth; cell proliferation;
 KW mammary tumour; oncogene; therapy; ds.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT CDS 188..2245
 FT /*tag= a
 PN WO9739357-A1.
 PD 23-OCT-1997.
 PF 11-APR-1997; U06049.
 PR 12-APR-1996; US-015307.
 PA (UJJO) UNIV JOHNS HOPKINS.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PI Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J,
 PI Nusse R, Samos CH, Wangy;
 DR WPI; 97-526631/48.
 DR P-PSDB; W31274.
 PT Identification of Wnt receptor binding modulators - useful for
 PT treatment of cancer and growth, development or proliferation related
 PT disorders
 PS Disclosure; Page 46-47; 61pp; English.
 CC This sequence comprises novel mouse frizzled gene 8 (Mfz8)
 CC that encodes a transmembrane receptor, frizzled-8 (see w31274),
 CC a Wnt receptor (WntR). Novel frizzled family members have been
 CC identified in Drosophila, mouse, human and Caenorhabditis (see
 CC T89885-92) and are considered to be Wnt receptors. Wnt receptors
 CC can be used in a novel, claimed method of screening for compounds
 CC which modulate the binding of a Wnt polypeptide (secreted proteins
 CC involved in cell-to-cell signalling) to a Wnt receptor. Wnt is
 CC involved in (mammary) cancer and other processes involving growth,
 CC development and proliferation (both normal and abnormal).
 CC Modulators identified by the claimed method are useful for
 CC treatment of diseases related to these conditions.
 SQ Sequence 2421 BP; 403 A; 772 C; 779 G; 467 T;
 Query Match 2.8%; Score 56; DB 37; Length 2421;
 Best Local Similarity 59.4%; Pred. No. 7.60e-15;
 Matches 177; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

Query Match 2.2%; Score 45; DB 32; Length 172;
Best Local Similarity 32.6%; Pred. NO. 3.11e-09;
Matches 42; Conservative 45; Mismatches 42; Indels 0; Gaps 0;

Query Match	2.2%	Score 45;	DB 32;	Length 172;
Best Local Similarity	32.6%	Pred. No. 3.11e-09;		
Matches	42;	Conservative	45;	Mismatches 42;
			Indels	0;
			Gaps	0
Db	11	bcbbbgcbtcbgbbtgcttctctcttcbggbtcbcbcttttbgcbtbggbbbcgct	70	
QY	208	CCTCTCCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTGCGCGGCCACGATGCTGCAGGC	267	
Db	71	gtbgtgcbgbbbtgtgtcttcbcttcbcbggbgtgcbgbbbtcbgbbggtgcgcb	130	
QY	268	CTGGCTCGCTCTGCTCTTCTCTCGCCTCGCACGTCTGCTTGGCTCGGCGCGCGG	327	
Db	131	gbgbgcbcb	139	
QY	328	CTCTTCTTC	336	

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RESULT      6
ID      N81164 standard; DNA; 204 BP.
ID      N81164; AC
DE      08-NOV-1990 (first entry)
DE      Base substituted E.coli beta-galactosidase alpha-fragment.
DE      E.coli beta galactosidase alpha-fragment; base substitutions; ss.
KW      Escherichia coli.
OS
Key
FH      Location/Qualifiers
FT      misc_feature
FT      19...69
FT      /*tag= a
FT      /function=multiple cloning site
FT      187..204
FT      primer_bind

```

PI Introducing random point mutations into nucleic acids -
PT by prep of single stranded template, annealing a primer, elongation,
PT misincorporation, completion of molecules and screening.
PT

disclosure: P; English.
Random point mutations were introduced into the alpha fragment of
E.coli beta-galactosidase. The wild type sequence was obtained as a
single stranded template and an oligonucleotide was hybridised to
it to generate a popn of DNA molecules which terminate at all
possible nucleotide positions within a specified region. The
variable 3' ends generated in this way are used as primers for
reverse transcriptase. Nucleotides are misincorporated by the
reverse transcriptase and the molecules are completed to forms that can be
amplified and then expressed in a suitable host-vector system.
The sequence covers all 176 diff base substitutions, most of which
occurred singularly in any given mutant.
See also P80575.
Sequence 204 BP; 21 A; 47 C; 17 G; 11 T; 108 Others;
Query Match 2.1%; Score 43; DB 1; Length 204;
Best Local Similarity 11.5%; Pred No. 3.03e-08;

A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisenase oligonucleotide (ON) to the airway epithelium of the subject. The present sequence is an antisenase oligonucleotide specific for the human IL4 receptor, targeted at the initiation codon. The method can be used to treat airway diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary disease, bronchitis and other airway diseases characterised by an inflammatory response. By eliminating

Query Match 2.0%; Score 40; DB 12; Length 114;
Best Local Similarity 9.1%; Pred. No. 8.76e-07;

Matches 10; Conservative 31; Mismatches 69; Indels 0; Gaps 0;

Ddb 5 gccnnbnbnbnbnbnbnbnbnbnbnbnbtgctgcnnbnbnbnbnbnbnbnbnbnbnbnbn 64
|| :
Qy 272 GCTCGTGCCTGCTCTTCCTCGCCTCGACTGCTGCTCGGTGGCTCGGCGCGGCTCT 331
:
Ddb 65 nbnnbnbnbnbnbnbnbnbnbtgcnnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbn 114
:
Qy 332 TCCTCTTTGGCCAGCCGCACTTCTCTACAAGCGACGAATTGCAAGCCC 381
:

RESULT 10
ID Q70468 standard; DNA; 114 BP.
AC Q70468;
DT 05-APR-1995 (first entry)
DE Generic DNA sequence to generate a random TSAR peptide library.
KW TSAR; totally synthetic affinity reagent; synthetic; binding domain;
KW effector domain; concatenated heterofunctional protein; linker;
KW direct; rapid; detection; screening; treatment; generic; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT misc_feature 55..60 /tag= a
FT FT /note= 'this sequence represents 'Z'; Z can be a
FT FT sequence of 6, 9 or 12 nucleotides (see
FT FT comments)'
PN WO9418318-A.
PD 18-AUG-1994. U00977.
PF 01-FEB-1994; US-013416.
PR 01-FEB-1993; US-013416.
PR 30-DEC-1993; US-176500.
PR 31-JAN-1994; US-189331.
PR (UYNC-) UNIV NORTH CAROLINA.
PI Fowlkes DM, Kay BK;
PA WPI: 94-279739/34.
DR P-PSDB: R65154.
PT Identifying proteins or peptide(s) which bind a ligand - by
PT screening a recombinant vector library expressing fusion proteins
PT comprising a binding domain and an effector domain
PS Disclosure; Page 35; 255pp; English.
CC Q70468 is a generic DNA sequence used to generate random TSAR (Totally
CC Synthetic Affinity Reagents) peptides.This generic formula can also be
CC represented as follows: X(NNB)Y((TGC)(NNB)62((NNB)77(TGC)(NNB))10Y. X
CC and Y are flanking restriction sites (X is not the same as Y) that are
CC not specified further. Other generic sequences are shown in Q70466-68.
CC Other specific peptides generated by these generic sequences are shown in
CC R65151-54. TSARs are concatenated heterofunctional proteins or peptides,
CC comprising at least two functional regions - a binding domain with
CC affinity for a ligand and a second effector peptide portion that is
CC chemically or biologically active.They may further comprise a linker
CC peptide between the 2 domains.The oligonucleotides are also designed so
CC that the expressed peptide contains 2 or 4 cysteine residues positioned
CC in, or flanking, the unpredicted or variant residues. These residues
CC confer some degree of conformational rigidity to the peptides. The TSARs
CC or compns. comprising a TSAR binding domain can be used in vivo to
CC deliver a chemically or biologically active moiety, eg. metal ion,
CC radioisotope, peptide, toxin or enzyme, to the specific target or on the
CC cell. They can also replace the function of macromolecules, eg.
CC monoclonal or polyclonal antibodies and therefore circumvent the need
CC for complex methods of hybridoma formation or in vivo antibody
CC production. The TSARs are easily characterised and have designed activity
CC allowing direct and rapid detection in a screening process.
SQ Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;

Query Match 2.0%; Score 40; DB 12; Length 114;
Best Local Similarity 5.4%; Pred. No. 8.76e-07;
Matches 6; Conservative 34; Mismatches 72; Indels 0; Gaps 0;

Ddb 3 bnbnnbnbnbnbnbnbnbnbnbnbnbnbtgcnnbnbnbnbnbnbnbnbnbnbnbnbn 62
:
Qy 199 CCGCCCTCGCCCTCCCCGGCTCGCTCTCTCTGCCCCCTCGGGGTGCGGCCACGATG 258
:
Ddb 63 bnbnnbnbnbnbnbnbnbnbtgcnnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbn 114


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FT W09418318-A. /note= "encoded by 2 (see comments)"
PN 18-AUG-1994.
PF 01-FEB-1994; U00977.
PR 01-FEB-1993; US-013416.
PR 30-DEC-1993; US-176500.
PR 31-JAN-1994; US-189331.
PA (UYNC-) UNIV NORTH CAROLINA.
PI Fowlkes DM, Key BK;
DR WPI: 94-279739/34.
DR P-PSDB: R58379.
PT Identifying proteins or peptide(s) which bind a ligand - by
PT screening a recombinant vector library expressing fusion proteins
PT comprising a binding domain and an effector domain
PS Disclosure: Page 36; 255pp; English.
CC Q70471 is a generic DNA sequence used to generate random TSAR (Totally
CC Synthetic Affinity Reagents) peptides. This generic formula can also be
CC represented as follows: X(NNB)6(CAC)(NNB)9(CAC)(NNB)2(CAC)(NNB)4(CAC)2
CC -(NNB)6(CAC)(NNB)(CAC)(NNB)2Y. X and Y are flanking restriction sites
CC (X is not the same as Y) that are not specified further. The peptides
CC generated by this and other generic sequences (Q70470-73) have invariant
CC histidine residues incorporated into variant sequences. TSARs are
CC concatenated heterofunctional proteins or peptides, comprising at least
CC two functional regions - a binding domain with affinity for a ligand and
CC a second effector peptide portion that is chemically or biologically
CC active. They may further comprise a linker peptide between the 2 domains.
CC The TSARs or compns. comprising a TSAR binding domain can be used in
CC vivo to deliver a chemically or biologically active moiety, eg. metal
CC ion, radioisotope, peptide, toxin or enzyme, to the specific target or
CC on the cell. They can also replace the function of macromolecules, eg.
CC monoclonal or polyclonal antibodies and therefore circumvent the need
CC for complex methods of hybridoma formation or in vivo antibody
CC production. The TSARs are easily characterised and have designed
CC activity allowing direct and rapid detection in a screening process.
SQ Sequence 114 BP; 7 A; 14 C; 0 G; 0 T;

Query Match 1.7%; Score 34; DB 12; Length 114;
Best Local Similarity 12.5%; Pred. No. 5.87e-04;
Matches 14; Conservative 28; Mismatches 70; Indels 0; Gaps 0;

Db 3 bnnbnnbnnbnnbcaacnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnna 62
QY 348 CGACTTCTCTACAGCGCAGCAATGTCAGCCCACTCCGCGCAACCTGCAGCTGTGCCA 407
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 cnbnnbnnbnnbcaacnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbn 114
QY 408 CGGCATCGAATACCAAGACATCGGCTGCCCACTGCTGGCCACGAGACC 459

RESULT 25
ID Q70465 standard; DNA; 114 BP.
AC Q70465;
DT 05-APR-1995 (first entry)
DE Generic DNA sequence to generate a random TSAR peptide library.
KW TSAR; totally synthetic affinity reagent; synthetic; binding domain;
KW effector domain; concatenated heterofunctional protein; linker;
KW direct; rapid; detection; screening; treatment; generic; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT misc_feature 55..60
FT /tag= a
FT /note= "This sequence represents '2'; 2 can be a
FT sequence of 6, 9 or 12 nucleotides (see
FT comments)"
PN W09418318-A.
PD 18-AUG-1994.
PF 01-FEB-1994; U00977.
PR 01-FEB-1993; US-013416.
PR 30-DEC-1993; US-176500.
PR 31-JAN-1994; US-189331.
PA (UYNC-) UNIV NORTH CAROLINA.
PI Fowlkes DM, Key BK;
DR WPI: 94-279739/34.

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DR P-PSDB; R65150 and R65151.
PT Identifying proteins or peptide(s) which bind a ligand - by
PT screening a recombinant vector library expressing fusion proteins
PT comprising a binding domain and an effector domain
PS Disclosure: Page 35; 255pp; English.
CC Q70465 is a generic DNA sequence used to generate random TSAR (Totally
CC Synthetic Affinity Reagents) peptides. This generic formula can also be
CC represented as follows: X(NNB)6(TGC)(NNB)11z(NNB)14(TGC)(NNB)3Y. X
CC and Y are flanking restriction sites (X is not the same as Y) that are
CC not specified further. Other generic sequences are shown in Q70466-68.
CC Other specific peptides generated by these generic sequences are shown in
CC R65151-54. TSARs are concatenated heterofunctional proteins or peptides,
CC comprising at least two functional regions - a binding domain with
CC affinity for a ligand and a second effector peptide portion that is
CC chemically or biologically active. They may further comprise a linker
CC peptide between the 2 domains. The oligonucleotides are also designed so
CC that the expressed peptide contains 2 or 4 cysteine residues positioned
CC in, or flanking, the unpredicted or variant residues. These residues
CC confer some degree of conformational rigidity to the peptides. The TSARs
CC or compns. comprising a TSAR binding domain can be used in vivo to
CC deliver a chemically or biologically active moiety, eg. metal ion,
CC radioisotope, peptide, toxin or enzyme, to the specific target or on the
CC cell. They can also replace the function of macromolecules, eg.
CC monoclonal or polyclonal antibodies and therefore circumvent the need
CC for complex methods of hybridoma formation or in vivo antibody
CC production. The TSARs are easily characterised and have designed
CC activity allowing direct and rapid detection in a screening process.
SQ Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;

Query Match 1.7%; Score 34; DB 12; Length 114;
Best Local Similarity 3.6%; Pred. No. 5.87e-04;
Matches 4; Conservative 33; Mismatches 75; Indels 0; Gaps 0;

Db 3 bnnbnnbnnbnnbgtcnnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnnnnn 62
Cp 630 GCACGGCTCTTACCTGCACGCGAGAGCGAGTGGCTGCTCGTAGGTC 571
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 bnnbnnbnnbnnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbnbn 114
Cp 570 ATCAGGCGACAGCGGGGCGAAGAGAGCGAGCAGCAGGAAGCTTCTTGGTCCGGG 519

RESULT 26
ID Q70471 standard; DNA; 114 BP.
AC Q70471;
DT 10-APR-1995 (first entry)
DE Generic DNA sequence to generate a random TSAR peptide library.
KW TSAR; totally synthetic affinity reagent; synthetic; binding domain;
KW effector domain; concatenated heterofunctional protein; linker;
KW direct; rapid; detection; screening; treatment; generic; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT misc_feature 55..60
FT /tag= a
FT /note= "encoded by 2 (see comments)"
PN W09418318-A.
PD 18-AUG-1994.
PF 01-FEB-1994; U00977.
PR 01-FEB-1993; US-013416.
PR 30-DEC-1993; US-176500.
PR 31-JAN-1994; US-189331.
PA (UYNC-) UNIV NORTH CAROLINA.
PI Fowlkes DM, Key BK;
DR WPI: 94-279739/34.
DR P-PSDB: R58379.
PT Identifying proteins or peptide(s) which bind a ligand - by
PT screening a recombinant vector library expressing fusion proteins
PT comprising a binding domain and an effector domain
PS Disclosure: Page 36; 255pp; English.
CC Q70471 is a generic DNA sequence used to generate random TSAR (Totally
CC Synthetic Affinity Reagents) peptides. This generic formula can also be
CC represented as follows: X(NNB)6(CAC)(NNB)9(CAC)(NNB)2(CAC)(NNB)4(CAC)2
CC -(NNB)6(CAC)(NNB)(CAC)(NNB)2Y. X and Y are flanking restriction sites

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T76445 standard; DNA; 264 BP.
AC T76445;
DT 16-SEP-1997 (first entry)
DE Substance P receptor antisense oligonucleotide.
KW Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW chronic obstructive pulmonary disease; bronchitis; ss.
OS Synthetic.
PN W09640162-A1.
PD 19-DEC-1996.
PF 06-JUN-1996; U09306.
PR 07-JUN-1995; US-474497.
PA (UYEC-) UNIV EAST CAROLINA.
PI Metzger WJ, Nyce JW;
DR WPI: 97-051871/05.
PT Treatment of airway diseases such as asthma - by topically applying
PT adenosine-free antisense oligo:nucleotide to airway epithelium of
PT subject 5; Page 40; 71pp; English.
CC A method for treating airway disease in a subject has been produced,
CC which involves the topical administration of an essentially adenosine
CC free antisense oligonucleotide (ON) to the airway epithelium of the
CC subject. The present sequence is an antisense oligonucleotide specific
CC for the substance P receptor, targeted at the initiation codon. The
CC method can be used to treat airway diseases such as cystic fibrosis,
CC asthma, chronic obstructive pulmonary disease, bronchitis and other
CC airway diseases characterised by an inflammatory response. By
CC eliminating adenosine from the antisense ON, its liberation upon
CC antisense degradation is prevented, thereby preventing adenosine-induced
CC bronchoconstriction in patients with hyper-reactive airways.
SQ Sequence 264 BP; 0 A; 72 C; 77 G; 56 T;

Query Match 1.6%; Score 32; DB 32; Length 264;
Best Local Similarity 37.8%; Pred. No. 4.74e-03;
Matches 31; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

Db 2 gctbgtgttcacccbtcbtcbbcggtgtccbcbbggtcbbcbbtgbcctg 61
|| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Qy 62 GCGCGGCTTCGACGCGCTCGCGCGGCTCTCCGCGTCTCCGCGCCAG 121
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 62 tbggcagctcccbbggcbcb 83
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Qy 122 CGCGCGCTGCCAGCTTCCTCGG 143
:| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT 33
ID T76170 standard; DNA; 88 BP.
AC T76170;
DT 12-SEP-1997 (first entry)
DE Human IL3 receptor antisense oligonucleotide.
KW Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW chronic obstructive pulmonary disease; bronchitis; interleukin; ss.
OS Synthetic.
PN W09640162-A1.
PD 19-DEC-1996.
PF 06-JUN-1996; U09306.
PR 07-JUN-1995; US-474497.
PA (UYEC-) UNIV EAST CAROLINA.
PI Metzger WJ, Nyce JW;
DR WPI: 97-051871/05.
PT Treatment of airway diseases such as asthma - by topically applying
PT adenosine-free antisense oligo:nucleotide to airway epithelium of
PT subject
PT Example 5; Page 28; 71pp; English.
CC A method for treating airway disease in a subject has been produced,
CC which involves the topical administration of an essentially adenosine
CC free antisense oligonucleotide (ON) to the airway epithelium of the
CC subject. The present sequence is an antisense oligonucleotide specific
CC for the human IL3 receptor, targeted at the initiation codon. The method
CC can be used to treat airway diseases such as cystic fibrosis, asthma,
CC chronic obstructive pulmonary disease, bronchitis and other airway
CC diseases characterised by an inflammatory response. By eliminating
CC adenosine from the antisense ON, its liberation upon antisense
CC degradation is prevented, thereby preventing adenosine-induced

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PR 07-JUN-1995; US-474497.
PI (UYEC-) UNIV EAST CAROLINA.
PI Metzger WJ, NYCE JW;
DR WPI: 97-051871/05.
PT Treatment of airway diseases such as asthma - by topically applying
PT adenosine-free antisense oligo:nucleotide to airway epithelium of
PT subject
PS Example 5; Page 40; 71pp; English.
CC A method for treating airway disease in a subject has been produced,
CC which involves the topical administration of an essentially adenosine
CC free antisense oligonucleotide (ON) to the airway epithelium of the
CC subject. The present sequence is an antisense oligonucleotide specific
CC for chymase, targeted at the initiation codon. The method can be
CC used to treat airway diseases such as cystic fibrosis, asthma, chronic
CC obstructive pulmonary disease, bronchitis and other airway diseases
CC characterised by an inflammatory response. By eliminating adenosine
CC from the antisense ON, its liberation upon antisense degradation is
CC prevented, thereby preventing adenosine-induced bronchoconstriction
CC in patients with hyper-reactive airways.
SQ Sequence 190 BP; 1 A; 41 C; 58 G; 36 T;

Query Match 1.5%; Score 31; DB 32; Length 190;
Best Local Similarity 42.9%; Pred. No. 1.32e-02;
Matches 30; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

Db 28 bbgbbccctgtbctcbbcgcttcgactctgctgcbgcbcbgbbgbbgcbgcbggbg 87
Cp 179 CGGGCCGCTCTCTTCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 121
Db 88 gbggbgbbgbbg 97
Cp 120 TGGGGCGCGG 111

RESULT 36
ID T76274 standard; DNA; 317 BP.
AC T76274;
DE 15-SEP-1997 (first entry)
DE Human neutrophil elastase (medullasin) antisense oligonucleotide.
KW Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW chronic obstructive pulmonary disease; bronchitis; ss.
OS Synthetic.
PN W09640162-A1.
PD 19-DEC-1996.
PF 06-JUN-1996; U09306.
PR 07-JUN-1995; US-474497.
PA (UYEC-) UNIV EAST CAROLINA.
PI Metzger WJ, NYCE JW;
DR WPI: 97-051871/05.
PT Treatment of airway diseases such as asthma - by topically applying
PT adenosine-free antisense oligo:nucleotide to airway epithelium of
PT subject
PS Claim 5; Page 33; 71pp; English.
CC A method for treating airway disease in a subject has been produced,
CC which involves the topical administration of an essentially adenosine
CC free antisense oligonucleotide (ON) to the airway epithelium of the
CC subject. The present sequence is an antisense oligonucleotide specific
CC for the human neutrophil elastase (medullasin), targeted at the
CC initiation codon. The method can be used to treat airway diseases
CC such as cystic fibrosis, asthma, chronic obstructive pulmonary disease,
CC bronchitis and other airway diseases characterised by an inflammatory
CC response. By eliminating adenosine from the antisense ON, its liberation
CC upon antisense degradation is prevented, thereby preventing adenosine-
CC induced bronchoconstriction in patients with hyper-reactive airways.
SQ Sequence 317 BP; 0 A; 112 C; 118 G; 36 T;

Query Match 1.5%; Score 30; DB 32; Length 317;
Best Local Similarity 41.0%; Pred. No. 3.65e-02;
Matches 73; Conservative 31; Mismatches 74; Indels 0; Gaps 0;

Db 79 ggcgcgcbtcbgbbgtggcgcbtcbggtgtggcgccgcbgbbgtggcctcgcbg 138
Cp 208 GCGGAGCGCGCGGAGTTCGAGCTGTCCCGGCGCCCTCTCTTCGCTGGTGGGACTCG 149

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Db 139 ctgcbgggbbcbcbtgbgbbggccbcgctggggcgctcgccgccccccbbbtctc 198
Cp 148 GGGCCCCGAAAGCTGGCAGCGCGGCTGGGGCGGAGAGCGGACACCGGGAGGAG 89
Db 199 cgbggcbgcbgctgcccccccbgcbgcbgcbgcbgcbgcbgcbgcbgcbgcb 256
Cp 88 CGCGGGCGGCGCTGCAAGCCCGCGCAGCTCCGGGGGGCTCCGACCCCGGGGAGC 31

RESULT 37
ID Q35072 standard; DNA; 565 BP.
AC Q35072;
DE 20-MAY-1993 (first entry)
DE HCV envelope region nucleic acid
DE Envelope; region; type C; hepatitis; virus; HCV; vaccine; serum;
KW non-A, non-B; amplify; ss.
OS Hepatitis C virus.
PN J04349885-A.
PD 04-DEC-1992.
PF 29-MAY-1991; 152169.
PR 29-MAY-1991; JP-152169.
PA (TEIJ ) TEIJIN LTD.
DR WPI: 93-022708/03.
DE Envelope region nucleic acid fragment - for type C hepatitis
PT virus (I), for producing vaccine
PT Claim 1; Page 2; 13pp; Japanese.
PS This sequence encodes a novel envelope region of type C hepatitis
CC virus (HCV). This fragment can be used for the preparation of a
CC vaccine for hepatitis C. This fragment was prepared from the serum
CC of non-A, non-B hepatitis patients and the envelope region DNA was
CC amplified by PCR using the primer sequences given in Q35073-76.
SQ Sequence 565 BP; 61 A; 92 C; 106 G; 85 T;

Query Match 1.5%; Score 30; DB 6; Length 565;
Best Local Similarity 26.5%; Pred. No. 3.65e-02;
Matches 41; Conservative 55; Mismatches 57; Indels 2; Gaps 2;

Db 219 gcwydyycbgbggtgryrbccytgtycgsgarrrryrryrryrryrryrryrry 278
Cp 206 GCCCTTCCCGGCTCCGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 265
Db 279 gctbacyccacgstygcrcyrcyrcyrcyrcyrcyrcyrcyrcyrcyrcyrcy 338
Cp 266 GCCCTGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 324
Db 339 yrtcgavtygctygtghggrsrgvrcyrcyrcyrcyrcyrcyrcyrcyrcyrcy 373
Cp 325 GGGCT-CTTCTCTTTGGCCAGCGCGGACTTCTCTCT 358

RESULT 38
ID N71302 standard; DNA; 3871 BP.
AC N71302;
DE 30-APR-1991 (first entry)
DE HSV-1 gB and surrounding regions.
KW vaccine; prophylaxis; treatment; Herpes Simplex Virus-1;
KW glycoprotein; gB; ss.
OS Herpes simplex virus type 1 (KOS).
PH Key Location/Qualifiers
FT misc_rna 1..375
FT /*tag= a
FT /*note= "5' extra sequences beginning with the XhoI
FT site"
FT caat_signal 406..410
FT /*tag= b
FT /*number= 1
FT caat_signal 443..448
FT /*tag= c
FT /*number= 2
FT tata_signal 476..479
FT /*tag= d
FT misc_rna 501..789

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Best Local Similarity 30.7%; Pred. No. 9.94e-02;
Matches 43; Conservative 44; Mismatches 52; Indels 1; Gaps 1;

Db 1 gbtgtttgttbcbbgcbtcbbgbbtbgcttgccttcttcbggtcbbtbtgcbcbtbb 60
   ||| | : : : | : : : ||| ||| : : | : : | : : | : : | : : |
Cp 196 GGAGTTGAGCTGTGCGGGCCGCTCTCTCTGCTGGGTGCGACTGGGGCCCGAAAA 137
   | : : : | : : : | : : | : : | : : | : : | : : | : : | : : |
Db 61 ggbtbbcgctgtgcbtcbgbbgtgcttbccttcbcbcbgcbgctgcb-gbbbtcbgg 119
   | : : : | : : : | : : | : : | : : | : : | : : | : : | : : |
Cp 136 GCTGAGCGCGCGCTGGCGCGGAGAGACCGGAGACCGGAGCGCGCGCGGAGGC 77
   : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 120 bbggtgcbcbgbbgcbcc 139
   : : | : : | : : | : : | : : | : : | : : | : : | : : |
Cp 76 GCTGCAAGCCGCGCGCAGC 57

RESULT 47
ID T76398 standard; DNA; 200 BP.
AC T76398;
DT 15-SEP-1997 (first entry)
DE Human leukotriene C4 synthase antisense oligonucleotide.
KW Asthma; airway epithelium; adenosine free; cystic fibrosis;
   chronic obstructive pulmonary disease; bronchitis; ss.
OS Synthetic.
PN W09640162-A1.
PD 19-DEC-1996.
PF 06-JUN-1996; U09306.
PR 07-JUN-1995; US-474497.
PA (UYEC-) UNIV EAST CAROLINA.
PI Metzger WJ, Nyce JW;
DR WPI: 97-051871/05.
PT Treatment of airway diseases such as asthma - by topically applying
   adenosine-free antisense oligo:nucleotide to airway epithelium of
   subject
PS Claim 5; Page 38; 7lpp; English.
CC A method for treating airway disease in a subject has been produced,
   which involves the topical administration of an essentially adenosine
   free antisense oligonucleotide (ON) to the airway epithelium of the
   subject. The present sequence is an antisense oligonucleotide specific
   for the human leukotriene C4 synthase, targeted at the initiation
   codon. The method can be used to treat airway diseases such as cystic
   fibrosis, asthma, chronic obstructive pulmonary disease, bronchitis
   and other airway diseases characterised by an inflammatory response.
   By eliminating adenosine from the antisense ON, its liberation upon
   antisense degradation is prevented, thereby preventing adenosine-
   induced bronchoconstriction in patients with hyper-reactive airways.
SQ Sequence 200 BP; 0 A; 53 C; 80 G; 32 T;

Query Match 1.4%; Score 28; DB 32; Length 200;
Best Local Similarity 44.1%; Pred. No. 2.67e-01;
Matches 56; Conservative 24; Mismatches 46; Indels 1; Gaps 1;

Db 1 ctgcgtgcbgcgcctgcbtcbggtggtgggc-csgtgggtgcbgcgcgcgcgcgbbg 59
   ||| | : : : | : : : ||| ||| : : | : : | : : | : : | : : |
QY 223 CTCCTCTGCCCCCTCGGGTCCGCCGCCACGATGTCGAGGCGCCCTGCTGCTG 282
   | : : : | : : : | : : | : : | : : | : : | : : | : : | : : |
Db 60 gcctgcgcgcgcgcbtcbggtgcbggbggtgcbggtgcbggtcctccbgbbg 119
   | : : : | : : : | : : | : : | : : | : : | : : | : : | : : |
QY 283 CTGCTTCTCTCCCTCGCACTGCTGCTGGGCTCGCGCGCGGCGCTTCCTTTGGC 342
   | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 120 gtbcbg 126
   | : : | : : | : : | : : | : : | : : | : : | : : | : : |
QY 343 CAGCCCG 349

RESULT 48
ID N82107 standard; cDNA; 1454 BP.
AC N82107;
DT 13-NOV-1990 (first entry)
DE PAP-I cDNA from human placenta, used for anticoagulant production..
KW PAP-I; anticoagulant; anti-inflammatory agent; phospholipid;
   phospholipase A2; disseminated intravascular coagulation; human placenta;
   deep vein thrombosis; ss.
```

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OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 13..972
FT /*tag= a
FT /product=PAP-I
PN WO805659-A.
PD 11-AUG-1988.
PF 05-FEB-1988; U00340.
PR 06-FEB-1987; US-011782.
PA (ZYMO-) Zymogenetics Inc; (UNIW) Univ of Washington.
PI Fujikawa K, Irani MH, Carter BLA;
DR WPI: 88-235049/33.
DR P-PSDB; P82317.
PT Human proteins having anticoagulant and antiinflammatory activity -
   isolated from biological fluid by anion-exchange chromatographoc media.
PS Disclosure; p; English.
CC A human placenta cDNA library (Clontech) was screened to obtain
   this sequence. The cDNA does not contain a leader peptide sequence,
   indicating that PAP-I is probably not constitutively secreted.
CC The product binds to phospholipid and inhibits phospholipase A2.
CC The protein can substitute heparin or other anticoagulants in
   the treatment of disseminated intravascular coagulation, deep vein
   thrombosis, or other disorders. It also has antiinflammatory
   properties.
SQ Sequence 1454 BP; 434 A; 280 C; 324 G; 416 T;

Query Match 1.4%; Score 28; DB 1; Length 1454;
Best Local Similarity 80.4%; Pred. No. 2.67e-01;
Matches 37; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 1227 atatatttttaaggaggtgagtgctttagcttttagccttttttaaaa 1272
   |||| | |||| | | | | | ||| |||| | |||| | |||| |
QY 1794 ATATAATTTTAAATTGACTTGACTTGACTTAAAGCCTTTTAAAA 1839

RESULT 49
ID N91353 standard; DNA; 1466 BP.
AC N91353;
DT 30-JUL-1989 (first entry)
DE Vascular anti-coagulating protein-alpha cDNA.
KW Vascular anti-coagulating proteins; hybridomas; B-cells; myelomas; ss.
FH Key Location/Qualifiers
FT cds 35..996
FT /*tag= a
FT /label=VAC-alpha cDNA
PN DE3810331-A.
PD 05-OCT-1989.
PF 26-MAR-1988; 810331.
PR 26-MAR-1988; DE-810331.
PA (BOEH) Boehringer Ingelhei.
PI Gunther A;
DR WPI: 89-293724/41.
DR P-PSDB; P91953.
PT Monoclonal antibodies to vascular anti-coagulating proteins - and
   hybridomas producing such antibodies.
PS Disclosure; fig 1; 1lpp; German.
CC The vascular anti-coagulating protein (VAC)-alpha encoded by this cDNA is
   injected into a host animal, in conjugation with eg keyhole limpet
   haemocyanin, and the B-cells from the immunised hosts are then fused with
   myeloma cells. The resultant hybridomas (VAA-8 and VAA-9) produce Abs
   specific to VAC-alpha. The Abs can be used as immunoassay reagents to
   detect VAC proteins, as affinity ligands for purificn. of VACs and as
   medicaments for binding and/or neutralising VAC proteins in vivo.
CC See also N91354 and EP-181465.
SQ Sequence 1466 BP; 423 A; 291 C; 327 G; 425 T;

Query Match 1.4%; Score 28; DB 2; Length 1466;
Best Local Similarity 80.4%; Pred. No. 2.67e-01;
Matches 37; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 1252 atatatttttaaggaggtgagtgctttagccttttttaaaa 1297
```

Qy 1794 ATATAAAATTTTATAATGACTTGACTACTTTAAAGCCTTGTTTAAAAA 1839
||||| ||||| ||| | || |||| |||| ||||| ||||| ||||| |||||

RESULT 50

ID N80801 standard; DNA; 1466 BP.
AC N80801;
DT 12-SEP-1990 (first entry)
DE Sequence encoding vascular anticoagulating protein (VAP) VAC-alpha
(Glu22)
KW Vascular anticoagulating protein (VAP) VAC-alpha; anticoagulant;
KW antinflammatory; phospholipase inhibitory.
OS Homo sapiens.
FH Key Location/Qualifiers
FT mat_peptide 35..997
FT /*tag= a
FT /note="claimed in claim 2, page 160-161"
PN WO8807576-A.
PD 06-OCT-1988.
PF 26-MAR-1988; E00266.
PR 04-NOV-1987; DE-737367.
PA (BOEH) Boehringer Ingelheimint.
PI Hauptmann R, Maurer-Fogy I, Bodo G, Swetly P, Stratowa C, Falkner E,
PI Adolf G, Reutlingsperger CMP;
DR WPI; 88-292861/41.
DR P-PSDB: P80714.
PT New vascular anti-coagulating proteins -
PT useful as thrombin inhibitors, antinflammatory agents, etc
PS Disclosure; Fig 4/1-4/3; 183pp; German.
CC The DNA is produced by determining the amino acid sequence of isolated
CC and highly purified VAPs, constructing through suitable cDNA libraries,
CC sequence, using the probes to search through suitable cDNA libraries,
CC isolating cDNA that hybridises with the probes, by inserting the cDNA
CC into a suitable vector, and using the vector to transform a host
CC organism. VAC-alpha has anticoagulant activity under certain
CC conditions, but loses this activity in the event of severe bleeding.
CC It acts by inhibiting conversion of factor X to factor Xa and conversion
CC of prothrombin to thrombin. It is structurally related to lipocortin I
CC (Nature, 320, 77, 1986) and lipocortin II (Cell, 46, 191/120, 1986) and
CC has similar antinflammatory and phospholipase inhibitory activity.
SQ Sequence 1466 BP; 422 A; 289 C; 328 G; 424 T; 3 Others;

Query Match 1.4%; Score 28; DB 1; Length 1466;
Best Local Similarity 80.4%; Pred. No. 2.67e-01;
Matches 37; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 1252 atatatatttttaagaggtagagtgcttttagccttttttaaaa 1297
||||| ||||| ||| | || |||| |||| ||||| ||||| |||||

Qy 1794 ATATAAAATTTTATAATGACTTGACTACTTTAAAGCCTTGTTTAAAAA 1839

RESULT 51

ID N81113 standard; DNA; 1567 BP.
AC N81113;
DT 12-NOV-1990 (first entry)
DE Plasmid contg. placental coagulation inhibitor gene.
KW Placental coagulation inhibitor; disseminated vascular coagulation;
KW thrombosis; ss.
FH Key Location/Qualifiers
FT cds 136..1098
FT /*tag= a
FT /label=placental coagulation inhibitor
FT /tag= b
PN EP-279459-A.
PN J03219875-A.
PD 24-AUG-1988.
PF 19-FEB-1988; 102468.
PR 23-JUL-1987; JP-184428.
PR 23-JUL-1987; JP-037227.
PA (KOWA) Kowa KK.
PI Saino Y, Iwasaki A, Suda M;
DR WPI; 88-236733/34.

DR WPI; 91-329110/45.
DR P-PSDB: P80511.
PT Recombinant placental coagulation inhibitor - useful for the prevention
PT and treatment of thromboses or disseminated intra-vascular coagulation.
PS Disclosure; P; English.
CC This recombinant DNA sequence comprises a promoter region, ribosome
CC binding site, initiation sequence, termination codon and a trans-
CC cription terminator in addition to the placental coagulation inhibitor
CC gene. The polypeptide produced on culturing of transformed host cells
CC exhibits strong anticoagulant activities and is useful for the treat-
CC ment and prevention of eg thrombosis or disseminated intravascular
CC coagulation in the brain, heart and peripheral blood vessels.
SQ Sequence 1567 BP; 430 A; 332 C; 358 G; 447 T;

Query Match 1.4%; Score 28; DB 1; Length 1567;
Best Local Similarity 80.4%; Pred. No. 2.67e-01;
Matches 37; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 1353 atatatatttttaagaggtagagtgcttttagccttttttaaaa 1398
||||| ||||| ||| | || |||| |||| ||||| ||||| |||||

Qy 1794 ATATAAAATTTTATAATGACTTGACTACTTTAAAGCCTTGTTTAAAAA 1839

RESULT 52

ID N90112 standard; DNA; 1575 BP.
AC N90112;
DT 1-NOV-1989 (first entry)
DE Anticoagulant PP4 DNA
KW Anticoagulant; PP4 protein; thromboplastin.
OS Homo sapiens (human)
FH Key Location/Qualifiers
FT poly_a_signal 1539..1575
FT /*tag= a
FT cds 107..1066
FT /*tag= b
PN EP-318703-A.
PD 07-JUN-1989.
PD 29-SEP-1988; 118039.
PR 03-NOV-1987; EP-737239.
PA (BEHW) Behringwerke AG.
PI Grundmann U, Abel K-J, Kupper H;
DR WPI; 89-166767/23.
PT New DNA sequence encoding anticoagulant PP4 protein
PT - and new recombinant protein, vectors, antibodies, etc.,
PT useful therapeutically and diagnostically.
PS Claim 1; Table 1; 14pp; German.
CC DNA sequence encoding anticoagulant PP4 protein. This
CC inhibits blood coagulation at the thromboplastin stage.
CC The derived protein is 320 amino acids.
SQ Sequence 1575 BP; 461 A; 322 C; 351 G; 441 T;

Query Match 1.4%; Score 28; DB 1; Length 1575;
Best Local Similarity 80.4%; Pred. No. 2.67e-01;
Matches 37; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 1324 atatatatttttaagaggtagagtgcttttagccttttttaaaa 1369
||||| ||||| ||| | || |||| |||| ||||| ||||| |||||

Qy 1794 ATATAAAATTTTATAATGACTTGACTACTTTAAAGCCTTGTTTAAAAA 1839

RESULT 53

ID N91821 standard; DNA; 1605 BP.
AC N91821;
DT 16-MAR-1990 (first entry)
DE Endonexin II complete cDNA
KW Placenta; blood coagulation.
OS Homo sapiens (human).
FH Key Location/Qualifiers
FT cds 160..1119
FT /*tag= a
PN EP-339285-A.
PD 02-NOV-1989.


```
PF 30-MAR-1989; 105636.
PR 31-MAR-1988; US-176802.
PA (RORE) Rorer Int Overseas.
PI Kapiian R, Jaye M;
DR P-PSDB; P91021.
PT Recombinant human endonexin II - which inhibits blood coagulation
PT and phospholipase A2 and is used as an antiinflammatory agent
PS Claim 1; fig. 1; 13pp; English.
CC hENI is a calcium and phospholipid binding protein.
SQ Sequence 1605 BP; 447 A; 337 C; 366 G; 455 T;

Query Match 1.4%; Score 28; DB 1; Length 1605;
Best Local Similarity 80.4%; Pred. No. 2.67e-01;
Matches 37; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Db 1378 atatatttttaagagctagctgttttagccttttttaaaa 1423
||||| ||||| ||| | ||||| ||||| ||||| |||||
QY 1794 ATATAAATTTTAAATGACTTGAGTACTTAAAGCCTTGTTAAAA 1839

RESULT 54
ID O65611 standard; cDNA; 1840 BP.
AC O65611;
DT 01-FEB-1995 (first entry)
DE Feline zona pellucida ZPB coding sequence.
KW Cat; feline; zona pellucida; ZPB; immunocontraception; ds.
OS Felis domesticus.
FH Key Location/Qualifiers
FT cds 57..1769
FT /*tag= a
FT /product= ZPB
PN W09411019-A.
PD 26-MAY-1994.
PF 06-NOV-1993; U10851.
PR 09-NOV-1992; US-973341.
PR 29-JAN-1993; US-012990.
PA (ZONA-) ZONAGEN INC.
PI Harris JD, Hsu KT, Podolski JS;
DR WPI; 94-183156/22.
DR P-PSDB; R55201.
PT Use of zona pellucida proteins and antibodies - for inducing
PT reproducible transient infertility or permanent sterility in
PT female mammals
PS Claim 24; Page 99-101; 154pp; English.
CC A cDNA library was prepared in lambda gt10 from mRNA isolated from
CC ovaries of 3-4 month old cats. Plaques were screened using a
CC mixture of probes encoding porcine ZPA, ZPB and ZPC proteins.
CC Positive clones were analysed further by Southern hybridisation
CC using the porcine probes and clones encoding feline ZPA, ZPB and
CC ZPC proteins were identified. The deduced amino acid sequence from
CC the feline ZPB clone was approximately 80% homologous to porcine ZPB
CC protein.
SQ Sequence 1840 BP; 433 A; 538 C; 441 G; 428 T;

Query Match 1.4%; Score 29; DB 11; Length 1840;
Best Local Similarity 96.8%; Pred. No. 9.94e-02;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1804 ttacacaaaaaataaaaaaaagcgccgc 1834
||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1997 TTACCTAAAAAATAAAAAAAGCGCGC 2027

RESULT 55
ID T89891 standard; DNA; 2259 BP.
AC T89891;
DT 27-APR-1998 (first entry)
DE Mouse frizzled gene 7 (Mfz7) encoding a Wnt receptor.
KW Wnt receptor; mouse frizzled gene 7; Mfz7 gene;
KW signal transduction; cancer; cell growth; cell proliferation;
KW mammary tumour; oncogene; therapy; ds.
OS Mus musculus.
```

```
FH Key Location/Qualifiers
FT CDS 361..2079
FT /*tag= a
FN W09739357-AL.
PD 23-OCT-1997.
PF 11-APR-1997; U06049.
PR 12-APR-1996; US-015307.
PA (UYJO ) UNIV JOHNS HOPKINS.
PA (STRD ) UNIV LELAND STANFORD JUNIOR.
PI Andrew D, Bhanot P, Brink M, Hsieh J, Nathans J,
PI Nusse R, Samos CH, Wangy;
DR WPI; 97-526631/48.
DR P-PSDB; W31273.
PT Identification of Wnt receptor binding modulators - useful for
PT treatment of cancer and growth, development or proliferation related
PT disorders
PS Disclosure; Page 43-44; 61pp; English.
CC This sequence comprises novel mouse frizzled gene 7 (Mfz7)
CC that encodes a transmembrane receptor, frizzled-7 (see W31273),
CC a Wnt receptor (WntR). Novel frizzled family members have been
CC identified in Drosophila, mouse, human and Caenorhabditis (see
CC T89885-92) and are considered to be Wnt receptors. Wnt receptors
CC can be used in a novel, claimed method of screening for compounds
CC which modulate the binding of a Wnt polypeptide (secreted proteins
CC involved in cell-to-cell signalling) to a Wnt receptor. Wnt is
CC involved in (mammary) cancer and other processes involving growth,
CC development and proliferation (both normal and abnormal).
CC Modulators identified by the claimed method are useful for
CC treatment of diseases related to these conditions.
SQ Sequence 2259 BP; 362 A; 739 C; 677 G; 481 T;

Query Match 1.4%; Score 29; DB 37; Length 2259;
Best Local Similarity 59.3%; Pred. No. 9.94e-02;
Matches 140; Conservative 0; Mismatches 93; Indels 3; Gaps 2;

Db 559 ctgcccacactgtgtggccacagaaacccagagagcggcgcttcgaggtgcaccagttc 618
||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 433 CTGCCCCAACCTGCTGGGCCACAGACCATGAAGAGAGTGTGGAGCGCGCTTGG 492
||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 619 tacctctgtgaaagtgccagtgcttcctcgtagctagctcttcttatgctctatgtac 678
||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 493 ATCCCGCTGTGTCATGAGCAGTGTCCACCCGACACCAAGAGTTCCTGTGCTGCTTTC 552
||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 679 gcaccogtgtgaccg-tg--ctcgaccagccattcctcgtgccccttccttctgtggag 735
||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 553 GCCCCCGCTGTGCTCGATGACCTAGACGAGACCATCAGCCATCCACTGCTGCTGTG 612
||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 736 cgtgcccgcagggctgctgagggcgctcatgaacaaagttcggcttcagtgccaga 791
||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 613 CAGGTGAAGGACCGCTGCGCCCGGTGTCATGCGCCTTCGGCTTCGCCGCCGA 668

RESULT 56
ID T76423 standard; DNA; 125 BP.
AC T76423;
DT 16-SEP-1997 (first entry)
DE Human endothelin ETA receptor antisense oligonucleotide.
KW Asthma; airway epithelium; adenosine free; cystic fibrosis;
KW chronic obstructive pulmonary disease; bronchitis; ss.
OS Synthetic.
PN W09640162-AL.
PD 19-DEC-1996.
PF 06-JUN-1996; US-474497.
PR 07-JUN-1995; US-09306.
PA (UYEC-) UNIV EAST CAROLINA.
PI Metzger WJ, Nyce JW;
DR WPI; 97-051871/05.
PT Treatment of airway diseases such as asthma - by topically applying
PT adenosine-free antisense oligo:nucleotide to airway epithelium of
PT subject
PS Example 5; Page 39; 71pp; English.
CC A method for treating airway disease in a subject has been produced,
CC which involves the topical administration of an essentially adenosine
```

[Logo: A stylized 'M' and 'S' inside a square frame, with 'M' on the left and 'S' on the right, both with vertical lines through them.]

(TM)

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Nov 5 10:57:48 1998; MasPar time 2269.27 Seconds
1370.520 Million cell updates/sec

Tabular output not generated.

Title: >US-08-848-439-1
Description: (1-2027) from US08848439.seq
Perfect Score: 2027
N.A. Sequence: 1 GAATTCGGCTTCATGCCT.....AAAAAAGGCGCGC 2027
Comp: CTTAAGCCGGAAGTACCGGA.....TTTTTTTTTTCGCGCGC

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 1988617 seqs, 767163441 bases x 2

Post-processing: Minimum Match 0%
Listing first 60 summaries

Database: embl-est55
Database: genbank-est107
3:gb_est1 4:gb_est10 5:gb_est11 6:gb_est12 7:gb_est13
8:gb_est14 9:gb_est15 10:gb_est16 11:gb_est17
12:gb_est18 13:gb_est19 14:gb_est20 15:gb_est21
16:gb_est22 17:gb_est23 18:gb_est24 19:gb_est25
20:gb_est26 21:gb_est27 22:gb_est28 23:gb_est29 24:gb_est30
25:gb_est31 26:gb_est32 27:gb_est33

Statistics: Mean 12.290; Variance 3.203; scale 3.837

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length	DB ID	Description
c 1	553	27.3	579	7	AA528226 nh92a05.s1 NCI_CGAP_Br
c 2	479	23.6	505	25	ze88f06.s1 Soares feta
c 3	472	23.3	480	22	Yy64d09.r1 Homo sapien
c 4	472	23.3	505	24	ze03g10.r1 Soares feta
c 5	468	23.1	473	8	nh88g03.s1 NCI_CGAP_Br
c 6	468	23.1	474	15	of62a09.s1 NCI_CGAP_Co
c 7	453	22.3	460	24	zd70e11.s1 Soares feta
c 8	434	21.4	443	17	xx08c06.s1 Soares tota
c 9	433	21.4	482	17	ch10h11.s1 NCI_CGAP_Co
c 10	425	21.0	427	5	zw51g08.s1 Soares tota
c 11	420	20.7	518	18	AA431859 NCI_CGAP_Co
c 12	416	20.5	446	22	Yy64d09.s1 Homo sapien
c 13	413	20.4	462	24	zd70e11.r1 Soares feta

c 14	409	20.2	409	7	AA449749	zx07e10.s1 Soares tota	0.00e+00
c 15	408	20.1	445	21	N32415	Yy63c06.s1 Homo sapien	0.00e+00
c 16	407	20.1	562	7	AA449032	zx07e10.r1 Soares tota	0.00e+00
c 17	405	20.0	405	8	AA505877	n101a05.s1 NCI_CGAP_Br	0.00e+00
c 18	402	19.8	408	17	AA976403	Qg68f09.s1 NCI_CGAP_Ki	0.00e+00
c 19	388	19.1	388	7	AA528219	nj16h09.s1 NCI_CGAP_Pr	0.00e+00
c 20	366	18.1	422	5	AA431858	zw51g08.r1 Soares tota	0.00e+00
c 21	366	18.1	458	25	AA105749	ml84a03.r1 Stratagene	0.00e+00
c 22	362	17.9	378	10	AA429960	zw58g10.r1 Soares tota	0.00e+00
c 23	363	17.9	378	10	AA429960	zw58g10.r1 Soares tota	0.00e+00
c 24	359	17.7	426	21	H87071	Yy74d07.r1 Homo sapien	0.00e+00
c 25	350	17.3	359	4	AA295018	EST100474 Pancreas tum	0.00e+00
c 26	330	16.7	349	18	AI047549	uh80b08.r1 Soares mous	0.00e+00
c 27	337	16.6	406	20	H16121	Yl28c05.r1 Homo sapien	0.00e+00
c 28	331	16.3	340	6	HUM296B07B	Human aorta cDNA 5'-en	0.00e+00
c 29	328	16.2	396	26	AA073862	mm97f07.r1 Stratagene	0.00e+00
c 30	329	16.2	414	23	AA024771	zf65g10.r1 Soares feta	0.00e+00
c 31	323	15.9	329	12	AA705737	zfx1b02.s1 Soares feta	0.00e+00
c 32	322	15.9	434	20	H44092	Yy73a07.r1 Homo sapien	0.00e+00
c 33	321	15.8	321	4	AA335712	EST40158 Epididymus Ho	0.00e+00
c 34	320	15.8	328	4	AA295688	EST100887 Pancreas tum	0.00e+00
c 35	321	15.8	469	20	H15818	Yl28c05.s1 Homo sapien	0.00e+00
c 36	319	15.7	326	21	N32424	Yw83e07.s1 Homo sapien	0.00e+00
c 37	316	15.6	330	6	HUM230F10B	Human aorta cDNA 5'-en	0.00e+00
c 38	313	15.4	344	22	N56835	Yw83c06.r1 Homo sapien	0.00e+00
c 39	299	14.8	301	6	HUM303B01B	Human aorta cDNA 5'-en	0.00e+00
c 40	301	14.8	301	10	AA603994	np31g01.s1 NCI_CGAP_Pr	0.00e+00
c 41	299	14.8	313	6	HUM304B12B	Human aorta cDNA 5'-en	0.00e+00
c 42	298	14.7	303	6	HUM347H05B	Human aorta cDNA 5'-en	0.00e+00
c 43	296	14.6	300	4	AA347786	EST54420 Fetal heart I	0.00e+00
c 44	294	14.5	300	6	HUM307G04B	Human aorta cDNA 5'-en	0.00e+00
c 45	292	14.4	302	4	AA330758	EST34493 Embryo, 6 wee	0.00e+00
c 46	290	14.3	293	6	HUM238C04B	Human aorta cDNA 5'-en	0.00e+00
c 47	290	14.3	293	6	HUM238C03B	Human aorta cDNA 5'-en	0.00e+00
c 48	290	14.3	344	20	H14917	Yl26d03.r1 Homo sapien	0.00e+00
c 49	287	14.2	289	6	HUM240B02B	Human aorta cDNA 5'-en	0.00e+00
c 50	285	14.1	287	6	HUM289F09B	Human aorta cDNA 5'-en	0.00e+00
c 51	279	13.8	281	6	HUM343G04B	Human aorta cDNA 5'-en	0.00e+00
c 52	273	13.5	273	6	HUM23G01B	Human aorta cDNA 5'-en	0.00e+00
c 53	274	13.5	276	5	AA371169	EST83193 Prostate gnan	0.00e+00
c 54	273	13.5	282	4	AA339113	EST44185 Fetal brain I	0.00e+00
c 55	269	13.3	283	6	C16543	Human aorta cDNA 5'-en	0.00e+00
c 56	256	12.6	262	25	AA176165	zp23h12.s1 Stratagene	0.00e+00
c 57	256	12.6	263	6	HUM286A04B	Human aorta cDNA 5'-en	0.00e+00
c 58	255	12.6	287	25	AA082155	ze88f06.r1 Soares feta	0.00e+00
c 59	255	12.6	394	26	AA260087	va52g08.r1 Soares mous	0.00e+00
c 60	254	12.5	266	6	HUM224H07B	Human aorta cDNA 5'-en	0.00e+00

ALIGNMENTS

RESULT 1
LOCUS AA528226 579 bp mRNA EST 05-AUG-1997
DEFINITION nh92a05.s1 NCI_CGAP_Br.1 Homo sapiens cDNA clone IMAGE:965936,
mRNA sequence.
ACCESSION AA528226
NID g2270295
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
Homo.
REFERENCE 1 (bases 1 to 579)
AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome
 Sequencing Center
 Clone Distribution: NCI-CGAP clone distribution
 information can be
 found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnli.gov/dbbr/image/image.html

Insert Length: 1268 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 206.

FEATURES	SOURCE
----------	--------

l: 1.379

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/organism="Homo sapiens"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from pooled bulk
breast tumor tissue, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is not normalized. (The normalized
version of this library is NCI-CGAP_Br_2." Library was
constructed by Bento Soares and M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone_lib="NCI-CGAP_Br1.1"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
1. ->579
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mrna	BASE COUNT	198 a	80 c	104 q	197 t
		<1.	>579		

Query Match 27.3%; Score 553; DB 7; Length 579;
Best Local Similarity 99.1%; Pred. No. 0.00e+00;
Matches 558; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db	17	TTTTTTTTTTTTTTTTTTAGGTAAACAGGAATGATAAGTTTATATACAAGATAATAATGTT	76
Cp	2019	TTTTTTTTTTTTTTTTTTAGGTAAACAGGAATGATAAGTTTATATACAAGATAATAATGTT	1960
Db	77	TATCTGAAATATTTACAGTGTGGTTAAAGCAATATTTTTACAACTTTTAAAGGTAACCT	136
Cp	1959	TATCTGAAATATTTACAGTGTGGTTAAAGCAATATTTTTACAACTTTTAAAGGTAACCT	1900
Db	137	ACTATGTATATTACAGGTAAAGTACAAATGGTTTAAATTTGCAAAAGTTAAAGTAAGAAATG	196
Cp	1899	ACTATGTATATTACAGGTAAAGTACAAATGGTTTAAATTTGCAAAAGTTAAAGTAAGAAATG	1840
Db	197	TTTTAAACRAAGGCTTAAAGTACTCAAGTCAATTAATAAATTTATATCTTTTGCCTTTTAC	256
Cp	1839	TTTTAAACRAAGGCTTAAAGTACTCAAGTCAATTAATAAATTTATATCTTTTGCCTTTTAC	1780
Db	257	TTGAAGAAATCATGCTATAGAAATGGTTAAATGTCCTCTTAATAAATGGAAGTATTGTAGC	316
Cp	1779	TTGAAGAAATCATGCTATAGAAATGGTTAAATGTCCTCTTAATAAATGGAAGTATTGTAGC	1720
Db	317	TGAAATGTGATACATGTAACAGATTTAAGTTCCTCCATTTGAAGGTATAAAATGATGAATGTT	376
Cp	1719	TGAAATGTGATACATGTAACAGATTTAAGTTCCTCCATTTGAAGGTATAAAATGATGAATGTT	1660
Db	377	GTAAGACTTTAGACACTGAGTCTCAGTCTGGAGCTGATGAAGATGTTGAGATAACACCCAG	436
Cp	1659	GTAAGACTTTAGACACTGAGTCTCAGTCTGGAGCTGATGAAGATGTTGAGATAACACCCAG	1600
Db	437	CTTTATCTCAACAGGTTTGTGACCCACAAGTTTGGGCCACAGAGAAAAATTTGAAGCCATT	496
Cp	1599	CTTTATCTCAACAGGTTTGTGACCCACAAGTTTGGGCCACAGAGAAAAATTTGAAGCAATT	1540
Db	497	TGCATGTTATGACAACCTCAGTGGGAAGTGAAATCCGCTGACTCAAAACCCACAAACAC	556
Cp	1539	TGCATGTTATGACAACCTCAGTGGGAAGTGAAATCCGCTGACTCAAAACCCACAAACAC	1480

Db 557 AACCAACCAGGCCCAAGTCCAG 579
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Cp 1479 AACCAACCAGACCCCAAGTCACAG 1457

RESULT	2	AA071469	505 bp	mRNA	EST	01-FEB-1997
LOCUS		ze88f06.s1	Soares fetal heart	NH9119W	Homo sapiens	cdna clone
DEFINITION		366083 3'	mRNA sequence.			

KEYWORDS
SOURCE

SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL COMMENT
-----------------	-------------------	-----------------------

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Fax: 314 280 1010
 Email: est@wustl.edu
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1171 Std Error: 0.00
 Seq primer: -40M13 fwd. from Amersham
 High quality sequence stop: 324

FEATURES
SOURCE

I. .303
/organism="Homo sapiens"
/note="Organ: heart; Vector: pTT73D (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCATCTCAAGTGGGACGGCCGCATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Patima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."
/db_xref="taxon:9606"
/clone="366083"
/clone_lib="Soares fetal heart NbHL19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
complement(<1..>505)

BASE COUNT	179 a	61 c	100 g	162 t	3 others
mrna					
complement(<1. .>505)					

Query Match 23.6%; Score 479; DB 25; Length 505;
Best Local Similarity 99.0%; Pred. No. 0.00e+00;
Matches 498; Conservative 0; Mismatches 2; Indels 3; Gaps 3;

Db	2	TAGTAAACAGAGATGAAAGTTTTATATACAGAATATAATGTTTATCTGAAATATTTC	61
Cp	2003	TAGTAAACAGGATGTAAGTTTATATACAGAATATAATGTTTATCTGAAATATTTC	1944
Db	62	AGTGTGGTTAAACGAATATTTTACAACTTTTAAAGGTAACACTACTGTATATTACAG	121
Cp	1943	AGTGTGGTTAAACGAATATTTTACAACTTTTAAAGGTAACACTACTGTATATTACAG	1884

FEATURES	Location/Qualifiers
source	1..480
/organism="Homo sapiens"	
/clone="278321"	
<1..>480	
mRNA	142 a 88 c 75 g 175 t
BASE COUNT	
ORIGIN	
Query Match	23.3%; Score 473; DB 22; Length 480;
Best Local Similarity	99.88; Pred. No. 0.00e+00;
Matches	479; Conservative 0; Mismatches 0; Indels 1; Gaps
Db 1	ATGAATATTTTATGAAGTTTAAATAGCTCACATTTAAAGCTAGTTTTGAATAGGTGCA 60
Qy 1396	ATGAATATTTTATGAAGTTTAAATAGCTCACATTTAAAGCTAGTTTTGAATAGGTGCA 1455
Db 61	ACTGTGACTTGGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Qy 1456	ACTGTGACTTGGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1515
Db 121	CCACTGAGGTGTCATAAAGCATCAAAATGCTTCAATTTTCTGTGGCCCAAACTTCTGG 180
Qy 1516	CCACTGAGGTGTCATAAAGCATCAAAATGCTTCAATTTTCTGTGGCCCAAACTTCTGG 1575
Db 181	GTCAACAAACCCCTGTCAGATAAAGCTGGCTGTTATCTCAACATCTTCATCAGCTCCAGAC 240
Qy 1576	GTCAACAAACCCCTGTCAGATAAAGCTGGCTGTTATCTCAACATCTTCATCAGCTCCAGAC 1635
Db 241	TGAGACTCAGTGCTTAAGTCTTACAAATTCATCATTTTATACCTTTCATGCGGAACCTTA 300
Qy 1636	TGAGACTCAGTGCTTAAGTCTTACAAATTCATCATTTTATACCTTTCATGCGGAACCTTA 1695
Db 301	AACGTGTACATGATACACATTCAGCTACATACATTCATTTTATAGAACACATTAACC 360
Qy 1696	AACGTGTACATGATACACATTCAGCTACATACATTCATTTTATAGAACACATTAACC 1755
Db 361	ATTTCATAGCATGATTTCTCAAGTAAAGCAAAAGATATAAATTTTATAATTGACTT 420
Qy 1756	ATTTCATAGCATGATTTCTCAAGTAAAGCAAAAGATATAAATTTTATAATTGACTT 1815
Db 421	GAGTACTTTAAGCCTTGGTTTAAACATTTCTTACTTAACTTTTGCAAATTAACCCATT 480
Qy 1816	GAGTACTTTAAGCCTTGG-TTTAAACATTTCTTACTTAACTTTTGCAAATTAACCCATT 1874
RESULT	4
LOCUS	w92531 505 bp mRNA EST 25-NOV-1996
DEFINITION	ze03g10.r1 Soares fetal heart NBHH19w Homo sapiens cDNA clone
357954 5', mRNA sequence.	
ACCESSION	w92531
NID	g1425099
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
Eukaryotae; mitochondrion eukaryotes; Metazoa; Chordata;	
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
REFERENCE	1 (bases 1 to 505)
AUTHORS	Hallier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
TITLE	The WashU-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu This clone is available royalty-free through UNITE. Contact the


```

Cp 1762 TAGAATGCTTAATGCTTCTAATAAATGAAGTATTAGCTGGAATGTGATACATGT 1703
|||||
Db 301 ACAGTTTAAGTCCCATTTGAAGGTATAAAATGATGAATGTTGTAAGACTTTAGACACTG 360
|||||
Cp 1702 AACAGTTTAAAGTCCCATTTGAAGGTATAAAATGATGAATGTTGTAAGACTTTAGACACTG 1643
|||||
Db 361 AGTCCCGTCTGGAGCTGATGAAGTGTGAGATACACGCCAGCTTTATCTCAACAGGTT 420
|||||
Cp 1642 AGTCTCAGTCTGGAGCTGATGAAGTGTGAGATACACGCCAGCTTTATCTCAACAGGTT 1583
|||||
Db 421 TTGTGACCCACCAAGTTTGGGCCCCAGAGAAAATTTGAAGCAAAATTTGCAATGTTA 472
|||||
Cp 1582 TTGTGACCCACCAAGTTTGGGCCCCAGAGAAAATTTGAAGCAAAATTTGCAATGTTA 1531
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RESULT 6
LOCUS AA857092 474 bp mRNA EST 09-MAR-1998
DEFINITION of62a09.s1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1434904 3',
mRNA sequence.
ACCESSION AA857092
NID 92945394
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 474)
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
TITLE Unpublished (1997)
JOURNAL
COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40mi3 fwd. ET from Amersham
High quality sequence stop: 464.
FEATURES
Location/Qualifiers
1..474
/organism="Homo sapiens"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
colon adenocarcinoma, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone="IMAGE:1434904"
/clone_lib="NCI_CGAP_Co8"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/lab 54 c 92 g 157 t

BASE COUNT 171 a 54 c 92 g
ORIGIN
source

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Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 474; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 AGGTAAACAGGATGTAAGTTTATATACAGAAATATATGTTTACTGAAATATTACA 60
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Cp 2002 AGGTAAACAGGATGTAAGTTTATATACAGAAATATATGTTTACTGAAATATTACA 1943
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Db 61 GTCTTGTTAAAGCAATATTTTACAACTTTTAAAGGTAACACTATGTATATACAGG 120
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Cp 1942 GTCTTGTTAAAGCAATATTTTACAACTTTTAAAGGTAACACTATGTATATACAGG 1893
|||||
Db 121 TAAGCTACAAATGGTGTAAATTTGCAAAAGTTAAGTAAGAAATGTTTAAACAAAGGCTTAA 180
|||||
Cp 1882 TAAGCTACAAATGGTGTAAATTTGCAAAAGTTAAGTAAGAAATGTTTAAACAAAGGCTTAA 1823
|||||
Db 181 AGTACTCAAGTCAATATAAAATTTATCTTTTGGCTTTTACTTTGAAGAAATCATGCTA 240
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Cp 1822 AGTACTCAAGTCAATATAAAATTTATCTTTTGGCTTTTACTTTGAAGAAATCATGCTA 1763
|||||
Db 241 TAGAAATGGTTAATGTCCTTCTAATAAATGGAAGTATTAGCTGGATGTGATACATGT 300
|||||
Cp 1762 TAGAAATGGTTAATGTCCTTCTAATAAATGGAAGTATTAGCTGGATGTGATACATGT 1703
|||||
Db 301 AACAGTTTAAAGTCCCATTTGAAGGTATAAAATGATGAATTTGTTGAAGACTTTAGACACTG 360
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Cp 1702 AACAGTTTAAAGTCCCATTTGAAGGTATAAAATGATGAATTTGTTGAAGACTTTAGACACTG 1643
|||||
Db 361 AGTCTCAGTCTGGAGCTGATGAAGTGTGAGATACACGCCAGCTTTATCTCAACAGGTT 420
|||||
Cp 1642 AGTCTCAGTCTGGAGCTGATGAAGTGTGAGATACACGCCAGCTTTATCTCAACAGGTT 1583
|||||
Db 421 TTGTGACC-ACAAAGTTGGGCCACAGAGAAAATTTGAAGCAAAATTTGCAATGTTATGA 474
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Cp 1582 TTGTGACCCACCAAGTTTGGGCCCCAGAGAAAATTTGAAGCAAAATTTGCAATGTTATGA 1528
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RESULT 7
LOCUS W72225 460 bp mRNA EST 17-OCT-1996
DEFINITION zd70e11.s1 Soares fetal heart NBHH19W Homo sapiens cDNA clone
346028 3', mRNA sequence.
ACCESSION W72225
NID g1382674
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 460)
REFERENCE Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
TITLE
JOURNAL
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1550 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 384.
FEATURES
Location/Qualifiers
1..460
/organism="Homo sapiens"
/note="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCGCATCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of

```


normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."

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/db_xref="taxon:9606"
/clone="346028"
/clone_lib="Soares fetal heart NbHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
complement(<1. .>460)

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Complement (S.I. : 400)			
BASE COUNT	164 a	55 c	87 g
ORIGIN	154 t		

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Query Match      22.3%; Score 453; DB 24; Length 460;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 459; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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Db	1	AAAGTTTATATACAGAATATTAATGTTTATCTGAATAATTACAGTGTGGTTAAAGCAA	60
Cp	1986	AAAGTTTATATACAGAATATTAATGTTTATCTGAATAATTACAGTGTGGTTAAAGCAA	1927
Db	61	TATTTTTACAACTTTTAAAGGTAACACTACTATGTATATTACAGGTAAGCTACAATGGSTT	120
Cp	1926	TATTTTTACAACTTTTAAAGGTAACACTACTATGTATATTACAGGTAAGCTACAATGGSTT	1867
Db	121	TAAATTTGCAAAAGTTAAGTAAGAAATGTTTTTAAACAAGGCTTAAAGTACTCAAGTCAATT	180
Cp	1866	TAAATTTGCAAAAGTTAAGTAAGAAATGTTTTTAAACAAGGCTTAAAGTACTCAAGTCAATT	1807
Db	181	ATAAAAATTATATCTTTTGGCTTTTACTTTGAGAANAATCATGCTATAGAAATGGTTAATGT	240
Cp	1806	ATAAAAATTATATCTTTTGGCTTTTACTTTGAGAANAATCATGCTATAGAAATGGTTAATGT	1747
Db	241	GCCTCTAAATAAATGGAAGTATTGTAGCTGGAATGTGATACATGTAACAGTTTAAAGTTCCTC	300
Cp	1746	GCCTCTAAATAAATGGAAGTATTGTAGCTGGAATGTGATACATGTAACAGTTTAAAGTTCCTC	1687
Db	301	ATTGAAGGTATAAATGATGAATTCGTTGTAGAACTTAGACACATGAGTCTCAGTCTGGAG	360
Cp	1686	ATTGAAGGTATAAATGATGAATTTGTTGTAGAACTTAGACACATGAGTCTCAGTCTGGAG	1628
Db	361	CTGATCAAGATGTTGAGATAACAGCCAGCTTTATCTCAACAGGGTTTGTGACCCACACAAGT	420
Cp	1627	CTGATCAAGATGTTGAGATAACAGCCAGCTTTATCTCAACAGGGTTTGTGACCCACACAAGT	1568
Db	421	TTGGGCCACAGAAAAATTTGAAGCAATTTGCGATGTTATGA	460
Cp	1567	TTGGGCCACAGAAAAATTTGAAGCAATTTGCGATGTTATGA	1528

RESULT	8
LOCUS	AA496300 443 bp mRNA EST
DEFINITION	zxc0c06.s1 Soares total fetus NB2HF8 9w Homo sapiens cDNA clone 785866 3', mRNA sequence.

ACCESSION	AA449300
NID	g2163149
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapi

Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
 Homo.
 1 (bases 1 to 443)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
 Moore, B., Schellenger, K., Stepien, M., Tan, F., Theisberg, B.,
 White, Y., Wyllie, T., Waterston, R. and Wilson, R.
 WashU-Merck EST Project 1997
 Unpublished (1997)

COMMENT

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Tel: 314 286 1810
Fax: 314 286 1810

Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available royalty-free through LANL; contact the
IMAGS Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 412

FEATURES	SOURCE
1. High Accuracy: The model achieves a high accuracy rate, consistently performing well across various datasets and tasks.	Model Performance Metrics
2. Scalability: The system is designed to handle large volumes of data and complex tasks, ensuring performance remains stable as the workload increases.	System Architecture
3. Interpretability: The model's decisions are transparent and explainable, allowing users to understand the underlying reasons for the results.	Model Explainability
4. Robustness: The system is resilient to noise and outliers, maintaining high performance even in less-than-ideal conditions.	Model Robustness
5. Efficiency: The model is optimized for fast processing times, ensuring that results are delivered quickly to the user.	Model Efficiency
6. Flexibility: The system can be adapted to different environments and tasks, providing a versatile solution for various applications.	Model Flexibility
7. Integration: The model seamlessly integrates with existing systems and workflows, facilitating easy adoption and use.	Model Integration
8. Security: The system implements robust security measures to protect data and ensure compliance with relevant regulations.	Model Security
9. Customization: The model can be tailored to meet specific user requirements, providing a personalized experience.	Model Customization
10. Support: Comprehensive documentation and user support are provided to ensure a smooth onboarding and ongoing use of the system.	Model Support

```

i.:.443
/organism="Homo sapiens"
/notes=Vector: pT7f3D-Pac (Pharmacia) with
polylinker; Site.1: Not I; Site.2: Eco RI
was prepared from mRNA obtained from pool
(total) fetus material with a Not I - Oli
TGTACCAATCTCAAGTGGAGGCGCGCTTAATTTTTTTC
Double-stranded cDNA was ligated to Eco R
(Pharmacia), digested with Not I and clone
and Eco RI sites of the modified pT7T3 ve
went through one round of normalization,
constructed by Bento Soares and M. Fatim
/db_xref="taxon:9606"
/clone="785866"
/clone_lib="Soares total fetus N52HF8 9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
complement(<1. >443)
/db_xref="GDB:5983485"
mRNA

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mRNA

BASE COUNT	153 a	47 c	83 q	160 t
/uu_xref= 955.9903463				

Query Match 21.48; Score 434; DB 7; Length 443;

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Best Local Similarity 99.5%;
Pred. No. 0.00e+00;
Matches 441; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db	1	TTTTTTTTTTTTTTTTTTAGGTAAACAGGATGTAAGTTTATATACAAGAAATATAATGTTTA	60
Cp	2017	TTTTTTTTTTTTTTTTTTAGGTAAACAGGATGTAAGTTTATATACAAGAAATATAATGTTTA	1958
Db	61	TCGAAATATTACAGTGTGGTTAAAGCAATATTTTTACAACATTTTAAAGGTAAACTAC	120
Cp	1957	TCGAAATATTACAGTGTGGTTAAAGCAATATTTTTACAACATTTTAAAGGTAAACTAC	1998
Db	121	TATGTATATTACAGGTAAAGTACAAATGGGTTTAAATTTGCAAAAGTTAAGTAAGAAATGTT	180
Cp	1897	TATGTATATTACAGGTAAAGTACAAATGGGTTTAAATTTGCAAAAGTTAAGTAAGAAATGTT	1838
Db	181	TTAAACAAGGCTTAAAGTACTCAAGTCAATTAATAATTTATATCTTTTGCCTTTACTTT	240
Cp	1837	TTAAACAAGGCTTAAAGTACTCAAGTCAATTAATAATTTATATCTTTTGCCTTTACTTT	1778
Db	241	GAAGAAATCATGCTATAGAAATGGTTAATGTGCTTCTAAATAAATGGAAGTATTGTAGCTG	300
Cp	1777	GAAGAAATCATGCTATAGAAATGGTTAATGTGCTTCTAAATAAATGGAAGTATTGTAGCTG	1718
Db	301	GAATGTGATACATGTAACAGTTTAAGTTCCCATTTGAAGGTATAAAATGATGAATGTGTGG	360
Cp	1717	GAATGTGATACATGTAACAGTTTAAGTTCCCATTTGAAGGTATAAAATGATGAATGTGTG	1659
Db	361	TAAGACTTAGACACTGGGTCTCAGTCTGGAGCTCATGAAGATGTTGAGATAACAGCCAGC	420
Cp	1658	TAAAGACTTAGACACTGAGTCTCAGTCTGGAGCTCATGAAGATGTTGAGATAACAGCCAGC	1599
Db	421	TTTATCTCAACAGGGTTTGTGAC	443
Cp	1598	TTTATCTCAACAGGGTTTGTGAC	1576

RESULT	LOCUS	AA922948	482 bp	mRNA	EST	09-JUN-1998
DEFINITION	ch10h11.s1	NCI-GAP_C08	Homo sapiens	CDNA clone	IMAGE:1457445	3
		similar to	TR:008862	008862	SECRETED	
					FRIZZLED RELATED PROTEIN	

SFRP-2. [2] TR:P97299 ;, mRNA sequence.

ACCESSION
AA922948
NID
g3070257
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 482)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

JOURNAL
COMMENT

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1350

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/dbp/image/image.html

Insert Length: 870 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 377.

Location/Qualifiers

1. 482

/organism="Homo sapiens"

/note="Organ: colon; Vector: pT7D3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
colon adenocarcinoma, and was then primed with a Not I -

oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73

vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."

/db_xref="taxon:9606"

/clone="IMAGE:1457445"

/clone_lib="NCI_CGAP_C08"

/tissue_type="adenocarcinoma"

/lab_host="DH10B"

BASE COUNT 103 a 119 c 127 g 133 t

ORIGIN

Query Match 21.4%; Score 433; DB 17; Length 482;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 434; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 10 AAAATATTCATGATTTTATTAGTTTCAATATTTCTACAGATTCGGGTGGGCTTTCCCTT 69

Cp 1406 AAAATATTCATGATTTTATTAGTTTCAATATTTCTACAGATTCGGGTGGGCTTTCCCTT 1347

Db 70 TAGGTGAAACAGCTATCCACTCTCTGGCCTTATACTCAGGAATGCTGGGGATGCAA 129

Cp 1346 TAGGTGAAACAGCTATCCACTCTCTGGCCTTATACTCAGGAATGCTGGGGATGCAA 1287

Db 130 ACGTGCAAAAGCGGGGAAGCTGCCAGCTGAGACTGGAGCAGCTAGGAGTGTGCTT 189

Cp 1286 ACGTGCAAAAGCGGGGAAGCTGCCAGCTGAGACTGGAGCAGCTAGGAGTGTGCTT 1227

Db 190 GGGACGCGGAGCTGAGATCCCGGACAGAAATGGTCAGCCGTGCTTGGAGCAGGCGTG 249

Cp 1226 GGGACGCGGAGCTGAGATCCCGGACAGAAATGGTCAGCCGTGCTTGGAGCAGGCGTG 1167

Db 250 TCGGAGCCATCAGGATGCGGGAAGCTAGCAGCTTGGGAATGCTCGGGAGATGCGC 309

Cp 1166 TCGGAGCCATCAGGATGCGGGAAGCTAGCAGCTTGGGAATGCTCGGGAGATGCGC 1107

Db 310 TTGAACCTCTCTGCCCCCTTCTGCCACCGCTTCACCGAGGTGATCACCCACCC 369

Cp 1106 TTGAACCTCTCTGCCCCCTTCTGCCACCGCTTCACCGAGGTGATCACCGCTCCCCACCC 1047

Db 370 TGTTCCTGTCCTCCATGACACAGATAGGGCGGTGTGATGTCGTCATCTCTCACAGGTGCAC 429

Cp 1046 TGTTCCTGTCCTCCATGACACAGATAGGGCGGTGTGATGTCGTCATCTCTCACAGGTGCAC 987

Db 430 TGCAAGCTGCTCTTG 444

Cp 986 TGCAAGCTGCTCTTG 972

RESULT 10

LOCUS AA431859 427 bp mRNA EST 22-MAY-1997

DEFINITION zw51908.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone

ACCESSION AA431859

NID g2115567

KEYWORDS EST.

SOURCE human.

ORGANISM

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo.

REFERENCE 1 (bases 1 to 427)

AUTHORS Hillier,D., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.

TITLE WashU-Merck EST Project 1997

JOURNAL Unpublished (1997)

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -41ml3 fwd. ET from Amersham

High quality sequence stop: 214.

FEATURES

source

1. 427

/organism="Homo sapiens"

/note="Vector: pT7D3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'

TGTACCAATCTCAAGTGGAGCGGCGCTAATTTTTTTTTTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

/db_xref="taxon:9606"

/clone="773630"

/clone_lib="Soares total fetus Nb2HF8 9w"

/dev_stage="8-9 weeks"

/lab_host="DH10B"

complement(<1..>427) 148 t

BASE COUNT 154 a 46 c 79 g 148 t

ORIGIN

Query Match 21.0%; Score 425; DB 5; Length 427;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 426; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 TTTTATAGGTAACACAGGATGTAAGTTTATATACAGATATATGTTTATCTGAATA 60

Cp 2008 TTTTATAGGTAACACAGGATGTAAGTTTATATACAGATATATGTTTATCTGAATA 1949

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Db 61 TTTACAGTGTGGTTAAAGCAATATTTTACAACTTTTAAAGGTAACACTACTATGTATAT 120
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Cp 1948 TTTACAGTGTGGTTAAAGCAATATTTTACAACTTTTAAAGGTAACACTACTATGTATAT 1889
|||||
Db 121 TACAGGTAAGCTACAAATGGGTTTAAATTTGCAAAAGCTTAAGTAAGAAATGTTTAAACAAG 180
|||||
Cp 1888 TACAGGTAAGCTACAAATGGGTTTAAATTTGCAAAAGCTTAAGTAAGAAATGTTTAAACAAG 1829
|||||
Db 181 GCTTAAAGTACTCAAGTCAATATAAAATTTATATCTTTTGGCTTTTACTTGAAGAAATC 240
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Cp 1828 GCTTAAAGTACTCAAGTCAATATAAAATTTATATCTTTTGGCTTTTACTTGAAGAAATC 1769
|||||
Db 241 ATGCTATAGAAGTGTAAATGCTTCAATAAATGGAAGTATTCTAGCTGGAATGTAT 300
|||||
Cp 1768 ATGCTATAGAAGTGTAAATGCTTCAATAAATGGAAGTATTCTAGCTGGAATGTAT 1709
|||||
Db 301 ACATGTAAACAGTTTAAAGTCCCATTTGAAGGTATAAAATGATGAATTTGTTAAAGACTTAG 360
|||||
Cp 1708 ACATGTAAACAGTTTAAAGTCCCATTTGAAGGTATAAAATGATGAATTTGTTAAAGACTTAG 1649
|||||
Db 361 ACATGTAGTCTCAGTCTGGAGCTGATGAAGATGTTGAGATAACAGCCAGCTTTATCTCAA 420
|||||
Cp 1648 ACATGTAGTCTCAGTCTGGAGCTGATGAAGATGTTGAGATAACAGCCAGCTTTATCTCAA 1589
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Db 421 CAGGGTT 427
|||||
Cp 1588 CAGGGTT 1582

RESULT 11
LOCUS AA927991 518 bp mRNA EST 23-JUN-1998
DEFINITION On47008.s1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1559823 3'
similar to TR:008862 008862 SECRETED FRIZZLED RELATED PROTEIN
SFRP-2. [2] TR:P97299 ;, mRNA sequence.
ACCESSION AA927991
NID 93076735
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 518)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel.: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 853 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 194.
Location/Qualifiers
1. 518
/organism="Homo sapiens"
/modified-Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
note: modified polylinker; 1st strand cDNA was prepared from
colon adenocarcinoma, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo.
```

```
/db_xref="taxon:9606"
/clone="IMAGE:1559823"
/clone_lib="NCI_CGAP_Co8"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
BASE COUNT 112 a 123 c 141 g 142 t
ORIGIN
Query Match 20.7%; Score 420; DB 18; Length 518;
Best Local Similarity 98.8%; Pred. No. 0.00e+00;
Matches 425; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db 10 AAAATATTATCATGATTTTATTAGTTTGAATATTTTACAAAGATTCGGGTGGGCTTTCCCTT 69
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Cp 1406 AAAATATTATCATGATTTTATTAGTTTGAATATTTTACAAAGATTCGGGTGGGCTTTCCCTT 1347
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Db 70 TAGGTGAAACACAGCTATCCACTCCCTGTGGCCCTTAACTCAGAAATGCTGGGGATGCAA 129
|||||
Cp 1346 TAGGTGAAACACAGCTATCCACTCCCTGTGGCCCTTAACTCAGAAATGCTGGGGATGCAA 1297
|||||
Db 130 ACGTCAAAAGGCGAGGGAAGCTGCCAGGCTGAGACTGGAGCAGTACAGTGTGCTT 189
|||||
Cp 1286 ACGTCAAAAGGCGAGGGAAGCTGCCAGGCTGAGACTGGAGCAGTACAGTGTGCTT 1227
|||||
Db 190 GGGNAACGGGAGCTGAGATCCGGGAGCAGAAATGCTAGCCCTGCTCTGGAGCAGGCCTG 249
|||||
Cp 1226 GGGNAACGGGAGCTGAGATCCGGGAGCAGAAATGCTAGCCCTGCTCTGGAGCAGGCCTG 1167
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Db 250 TCGGAGCCATCAGGATCGCGGAGCTAGCAGCTGCAGCTTGGCGATGCTGGGAGATGCCG 309
|||||
Cp 1166 TCGGAGCCATCAGGATCGCGGAGCTAGCAGCTTGGCGATGCTGGGAGATGCCG 1107
|||||
Db 310 TTGAATCTCTCTGCCCCCTTCTGCCACCGCTTCGACGAGGTGATCACCAGCTCCCCACCC 369
|||||
Cp 1106 TTGAATCTCTCTGCCCCCTTCTGCCACCGCTTCGACGAGGTGATCACCAGCTCCCCACCC 1047
|||||
Db 370 TGTTTCTCTCCATGACCAGATAGGGCGCGTTTATGTCGTTTCATCTACTCAGGTGCAC 429
|||||
Cp 1046 TGTTTCTCTCCATGACCAGATAGGGCGCGTTGATGTCGTTTCATCTCTCAGAGGTGCAC 987
|||||
Db 430 TGAAGCTGT 439
|||||
Cp 986 TGAAGCTGT 977
|||||
RESULT 12
LOCUS N64004 446 bp mRNA EST 01-MAR-1996
DEFINITION YY64d09.s1 Homo sapiens cDNA clone 278321 3'.
ACCESSION N64004
NID g1211833
KEYWORDS EST.
SOURCE human clone=278321 primer=ml3 -40 forward library=Soares multiple
sclerosis 2NbHSP vector-pT73D (Pharmacia) with a modified
polylinker V-riPE: phagemid host=DH10B (ampicillin resistant)
Rsite=Not I Rsite=Eco RI 46 year old male. 1st strand cDNA was
primed with a Not I - oligo(dT) primer
[5'-TGTTTACCATCTGAAGTGGGCGCGCATTTTGTGTTTGTGTTTGTGTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I and Eco
RI sites of a modified pT7 vector (Pharmacia). Library went
through one round of normalization to a Cot = 5. Library
constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4
multiple sclerosis lesions from one patient was kindly provided by
Dr. Kevin G. Becker (NINDS/NIH).
ORGANISM Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 446)
REFERENCE Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlring,T., Soares,M., Tan,F.,
```


Db 363 CCAAGACAGACCATTTACAGCTGAACGGTGTGTGTCGGAAGGACCTTGAAGAAATCG 422
|||||
Qy 902 CCAAGACAGACCATTTACAGCTGAACGGTGTGTGTCGGAAGGACCTTGAAGAAATCG 960
|||||

Db 423 GTGCTGTGGCTCAAGACAGCTTCGAGTGCACCTGTGA 460
|||||
Qy 961 GTGCTGTGGCTCAAGACAGCTTCGAGTGCACCTGTGA 998
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RESULT 14
LOCUS AA449749 409 bp mRNA EST 04-JUN-1997
DEFINITION zk07e10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone
78502 3', mRNA sequence.
ACCESSION AA449749
NID g2163499
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominae;
Homo.

REFERENCE 1 (bases 1 to 409)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE WashU-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 408.
Location/Qualifiers
I. .409
/organism="Homo sapiens"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGGCGCGCTAAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone="785802"
/clone_lib="Soares total fetus Nb2HF8 9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
complement(<1.>409)
/db_xref="GDB:5983421"
BASE COUNT 148 a 42 c 75 g 144 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TTTTCTTTAGTAAACAGGATGATAAGCTTTATATACAGAATAATATGTTTCTGAAA 60
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Cp 2010 TTTTCTTTAGTAAACAGGATGATAAGCTTTATATACAGAATAATATGTTTCTGAAA 1951
|||||

Db 61 TATTACAGTGTGGTTAAAGCAATATTTTACAACTTTTAAAGGTAACACTATGTAT 120
|||||

Cp	1950	TATTACAGTGTGGTTTAAGCAATATTTTTTACAACTTTTAAAGGTAACACTACTATGTAT	1891
Db	121	ATTACAGGTAAGCTACAATGGGTTTAAATTTGCAAAAGTTAAAGTAAGAAATGTTTTAAACA	180
Cp	1890	ATTACAGGTAAGCTACATGGGTTTAAATTTGCAAAAGTTAAAGTAAGAAATGTTTTAAACA	1831
Db	181	AGGCTTAAAGTACTCAAGTCAATTTATAAAATTTATATCTTTTGGCCCTTTTACTTTGAAGAAA	240
Cp	1830	AGGCTTAAAGTACTCAAGTCAATTTATAAAATTTATATCTTTTGGCCCTTTTACTTTGAAGAAA	1771
Db	241	TCATGCTATAGAATGGTTAAATGCTCTCTATATAATGGAAGTATTTGAGCTGGAATGTG	300
Cp	1770	TCATGCTATAGAATGGTTAAATGCTCTCTATATAATGGAAGTATTTGAGCTGGAATGTG	1711
Db	301	ATACATGTAACAGTTTAAAGTTCCCATTTGAAGGTATATAAATGATGAATTTGTTAAAGACTT	360
Cp	1710	ATACATGTAACAGTTTAAAGTTCCCATTTGAAGGTATATAAATGATGAATTTGTTAAAGACTT	1651
Db	361	AGACACTGAGTCTCAGTCTGGAGCTGATGAAGATGTTGAGATAACAGCC	409
Cp	1650	AGACACTGAGTCTCAGTCTGGAGCTGATGAAGATGTTGAGATAACAGCC	1602
RESULT	15		
LOCUS	N32415	445 bp	mrna
DEFINITION	YW83C06.s1 Homo sapiens	cdna clone	258826 3'
ACCESSION	N32415		
NID	g1152814		
KEYWORDS	EST.		
SOURCE	human clone=258826 primer=wl3 -40 forward library=Soares placenta 8to9weeks 2NHP8to9W vector=pf7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI two placentae: one from 8 weeks and another from 9 weeks post conception. 1st strand cdna was primed with a Not I - oligo(dT) primer [5'-TCTTACCAATCTGAAGTGGAGCGCGGATTTTCTTTTCTTTT-3'], double-stranded cdna was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pf7T3 vector (Pharmacia). Library constructed by Bento Soares and M. Fatima Bonaldo.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 445) Hallier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kuceba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.		
TITLE	The WashU-Merck EST Project		
JOURNAL	Unpublished (1995)		
COMMENT	Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 314 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Location/Qualifiers 1. .445 /organism="Homo sapiens" /clone="258826" <1. .445		
FEATURES	source		
BASE COUNT	156 a	87 g	147 t
ORIGIN			

Query Match 20.1%; Score 408; DB 21; Length 445;

Best Local Similarity 98.6%; Pred. No. 0.00e+00;

Matches 434; Conservative 0; Mismatches 2; Indels 4; Gaps 4;

Db 1 AAACAGGATGAAAGTTTATATACAGATATAAATGTTTATCTGAAATATTTACAGTGT 60

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Cp 1998 AAACAGGATGAAAGTTTATATACAGATATAAATGTTTATCTGAAATATTTACAGTGT 1939

|||||

Db 61 TGGTTAAAGCAATATTTTACAACTTTTAAAGTAACTACTATGATGATATTTACAGGTAAG 120

|||||

Cp 1938 TGGTTAAAGCAATATTTTACAACTTTTAAAGTAACTACTATGATGATATTTACAGGTAAG 1879

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Db 121 CTACAATGGGTTTAAATTCGAAAGTTAAGTAAAGAAATGTTTAAACAAGGCTTAAAGTA 180

|||||

Cp 1878 CTACAATGGGTTTAAATTCGAAAGTTAAGTAAAGAAATGTTTAAACAAGGCTTAAAGTA 1819

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Db 181 CTCAGTCAATTAATAATTTATATCTTTTGCCCTTTTACTTGAAGAAATCATGCTATAGA 240

|||||

Cp 1818 CTCAGTCAATTAATAATTTATATCTTTTGCCCTTTTACTTGAAGAAATCATGCTATAGA 1759

|||||

Db 241 AATGGTTAATGCTCTCTAATAATGAAGTATTTAGCTGGAATGATGATGATGATGATAACA 300

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Cp 1758 AATGGTTAATGCTCTCTAATAATGAAGTATTTAGCTGGAATGATGATGATGATGATAACA 1699

|||||

Db 301 GTTTAAGTCCCATTTGAAGTATAAATGATGAATTTGTTGAAGACTTAGACACTGGAGT 360

|||||

Cp 1698 GTTTAAGTCCCATTTGAAGTATAAATGATGAATTTGTTGAAGACTTAGACACTGGAGT 1640

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Db 361 CTCAGTCTGGAGCTGATGAAGATGTTGAGATAACAGCCAGCTTTATCCCAACAGGGGT 420

|||||

Cp 1639 CTCAGTCTGG-AGCTGATGAAGATGTTGAGATAACAGCCAGCTTTATCTC-AACAGGG-T 1583

|||||

Db 421 TTGTGACCCACAGTTTGG 440

|||||

Cp 1582 TTGTGACCCACAGTTTGG 1563

RESULT 16

LOCUS AA449032 562 bp mRNA EST 04-JUN-1997
DEFINITION zx07e10.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 785802 5' similar to TR:G310115 G310115 FRIZZLED PROTEIN HOMOLOG 2
PRECUSOR ; mRNA sequence.

ACCESSION AA449032

NID G2163052

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)

TITLE

JOURNAL

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 467.

FEATURES

source

1..562
/organism="Homo sapiens"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I - oligo(dT) primer [5' TGTACATCTGAAAGTGAAGGAGCGCGCTAATTTTATTTT 3'].

Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

/db_xref="taxon:9606"

/clone="785802"

/clone_lib="Soares total fetus Nb2HF8 9w"

/dev_stage="8-9 weeks"

/lab_host="DH108"

<1..>562

/db_xref="GDB:5983421" 98 t

BASE COUNT 75 a 232 c 157 g

ORIGIN

Query Match 20.1%; Score 407; DB 7; Length 562;

Best Local Similarity 98.2%; Pred. No. 0.00e+00;

Matches 440; Conservative 0; Mismatches 3; Indels 5; Gaps 5;

Db 1 GCTCATCTCTCCCCGGGTGCGAGCCCCCGGAGCTGCGCGGGGCTTGCAGCGC-TC 59

|||||

Qy 22 GCTCATCTCTCCCCGGGTGCGAGCCCCCGGAGCTGCGCGGGGCTTGCAGCGCCTC 81

|||||

Db 60 GCGCGCTGCTCTCCCGGTGTCGCGCTTCTCCGCGCCCCAGCCGCGG-TCGCCAGCTTTT 118

|||||

Qy 82 GCGCGGC-TCCTCCCGGTGTCGCGCTTCTCCGCGCCCCAGCCGCGGCTGCCAGCTTTT 140

|||||

Db 119 CGGGCCCCGAGTCGACCCAGCAGAGAGCGGGCGGGGAGAGCTCGCACTCCGGCC 178

|||||

Qy 141 CGGGCCCCGAGTCGACCCAGCAGAGAGCGGGCGGGGAGAGCTCGCACTCCGGCC 200

|||||

Db 179 GCCTCGCCCTTCCCGGCTCGGCTCCTCTGCCCTCGGG-TCGCGGGCCACGATGCT 237

|||||

Qy 201 GCCTCGCCCTTCCCGGCTCGGCTCCTCTGCCCTCGGGGTCGCGGGCCACGATGCT 260

|||||

Db 238 GCAGGGCCCTGGCTGCTGCTGCTCTTCTCGCTCGCACTGCTGCTGGGCTCGGC 297

|||||

Qy 261 GCAGGGCCCTGGCTGCTGCTGCTCTTCTCGCTCGCACTGCTGCTGGGCTCGGC 320

|||||

Db 298 GCGGGGCTCTTCTCTTTTGGCCAGCCCGACTTCTCTACAGGCGAG-AATTGCAAGCC 356

|||||

Qy 321 GCGGGGCTCTTCTCTTTTGGCCAGCCCGACTTCTCTACAGGCGAGCAATTGCAAGCC 380

|||||

Db 357 CATCCCTGCCAACTGCGAGCTGTCACGCGCATCGAATACAGACATGCGGCTGCCCAA 416

|||||

Qy 381 CATCCCGCCAACTGCGAGCTGTCACGCGCATCGAATACAGACATGCGGCTGCCCAA 440

|||||

Db 417 CTGCTGGGCGCAGAGACCATGAAGCAG 444

|||||

Qy 441 CTGCTGGGCGCAGAGACCATGAAGCAG 468

|||||

RESULT 17

LOCUS AA505877 405 bp mRNA EST 20-AUG-1997

DEFINITION ni01a05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:966704, mRNA sequence.

ACCESSION AA505877

NID G2242014

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 405)

AUTHORS NCI-CGAP

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

Db 360 CTGTGACTTGCGTCTGGTTGGTTGTTGTTGTTGTTGTTGAGTCACGCTGA 408
|||||
QY 1457 CTGTGACTTGCGTCTGGTTGGTTGTTGTTGTTGTTGTTGAGTCACGCTGA 1505
|||||

RESULT 19
LOCUS AA528219 388 bp mRNA EST 05-AUG-1997
DEFINITION n16109.s1 NCI_CGAP_P-22 Homo sapiens cDNA clone IMAGE:986561, mRNA sequence.
ACCESSION AA528219
NID g2270288
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo.

REFERENCE 1 (bases 1 to 388)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 465 Std Error: 0.00
Seq Primer: -40ml3 fwd ET from Amersham.
Location/Qualifiers
1..388
/organism="Homo sapiens"
/note="Organ: prostate; Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with a Not I - EcoRI primer. Double-stranded cDNA was ligated to oligo(R) adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone_image="IMAGE:986561"
/clone_lib="NCI_CGAP_Pr22"
/sex="male"
/tissue_type="normal prostate"
/lab_host="DH10B"
BASE COUNT 143 a 39 c 72 g 134 t
ORIGIN
Query Match 19.1%; Score 388; DB 7: Length 388;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 388; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 AGGTAAACAGGATGTAAGTTTATACAGAATAAATGTTTATCTGAAATATTACA 60
|||||
Cp 2002 AGGTAAACAGGATGTAAGTTTATACAGAATAAATGTTTATCTGAAATATTACA 1943
|||||

Db 61 GTGTGGTTAAAGCAATATTTTTACAACTTTTAAAGGTAACACTACTATGTATATATACAGG 120
|||||
Cp 1942 GTGTGGTTAAAGCAATATTTTTACAACTTTTAAAGGTAACACTACTATGTATATATACAGG 1893
|||||

Db 121 TAAGCTACATGGGTTTAATTTGCCAAAGTTAAGTAGAANAATGTTTTAAACAAGGCCTTAA 180
|||||

Best Local Similarity 99.7%; Pred. No. 0.00e+00;
Matches 372; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 51 CTAGTCCCGGATCCTGATGCTCCGACAG-CCTGCTCCAGACACGGCTGACCATTTCT 109
      |||
QY 1140 CTAGTCCCGGATCCTGATGCTCCGACAGGCTGCTCCAGACAGGCTGACCATTTCT 1199
      |||
Db 110 GTCCTGGGATCTAGCTCCGTTCCGACAGCACACTGCTAGCTGCTCAGCTCAGCGTG 169
      |||
QY 1200 GTCCTGGGATCTAGCTCCGTTCCGACAGCACACTGCTAGCTGCTCAGCTCAGCGTG 1259
      |||
Db 170 GGCAGCTTCCCTGCTGCTTTGACGTTTGATCCATCCAGCATTTCCTGAGTTAAGGCC 229
      |||
QY 1260 GGCAGCTTCCCTGCTGCTTTGACGTTTGATCCATCCAGCATTTCCTGAGTTAAGGCC 1319
      |||
Db 230 ACAGGAGTGGATAGCTGTTTTCACCTAAAGGAAAGCCACCCGAAATCTGTAGAAATAT 289
      |||
QY 1320 ACAGGAGTGGATAGCTGTTTTCACCTAAAGGAAAGCCACCCGAAATCTGTAGAAATAT 1379
      |||
Db 290 TCAACTAATAAATCATGATATTTTATGAAGTTTAAATAAGCTCACCTTAAAGCTA 349
      |||
QY 1380 TCAACTAATAAATCATGATATTTTATGAAGTTTAAATAAGCTCACCTTAAAGCTA 1439
      |||
Db 350 GTTTTGAATAGTCAACTGCTGACTTGGTCTGCTGGTGTGTTGTTGTTTGTGATC 409
      |||
QY 1440 GTTTTGAATAGTCAACTGCTGACTTGGTCTGCTGGTGTGTTGTTGTTTGTGATC 1499
      |||
Db 410 AGCTGATTTTCAC 422
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QY 1500 AGCTGATTTTCAC 1512
      |||
```

```
RESULT 21
LOCUS AA105749 458 bp mRNA EST 04-FEB-1997
DEFINITION ml84a03.r1 Stratagene mouse kidney (#937315) Mus musculus CDNA
clone 518668 5', similar to TR:G1151260 G1151260 TRANSMEMBRANE
RECEPTOR. ; mRNA sequence.
ACCESSION AA105749
NID g1654838
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
REFERENCE 1 (bases 1 to 458)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisli,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
TITLE Contact: Marra M/Mouse EST Project
JOURNAL WashU-HMI Mouse EST Project
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:312516
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 457.
Location/Qualifiers
1. .458
/organism="Mus musculus"
/strain="C57/B16"
/note="vector: Bluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dt. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
```

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sequence: 5' GAATTCGACGAG 3' -3' adaptor sequence: 5'
CTGAGCTTTTCTTTTCTTTT 3'
/db_xref="taxon:10090"
/clone="518668"
/clone_lib="Stratagene mouse kidney (#937315)"
/sex="females"
/dev_stage="4 weeks"
/lab_host="SOLR (kanamycin resistant)"
<1..>458
mRNA 119 a 140 c 116 g 83 t
BASE COUNT
ORIGIN
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Query Match 18.1%; Score 356; DB 25; Length 458;
Best Local Similarity 91.8%; Pred. No. 0.00e+00;
Matches 424; Conservative 0; Mismatches 34; Indels 4; Gaps 4;
Db 1 AGCAGGCGGGCGATGATTCGCTGTCATGAAGCAGTGCACCGGACACCAAGAAGT 60
      |||
QY 476 AGCAGGCGGGCGCTTGGATCCGCTGGTCAAGCAGTGCACCGGACACCAAGAAGT 535
      |||
Db 61 TCCTGTGCTGCTCTTCGCCCTGCTCTCTCGACGACTAGATGAGACCATCCAGCGT 120
      |||
QY 536 TCCTGTGCTGCTCTTCGCCCTGCTCTCTCGACGACTAGATGAGACCATCCAGCAT 595
      |||
Db 121 GTCACTGCTCTG-GTGCAGTGAAGACCGTGGGCCCCGGTCAATGTCGGCTTCG-CT 178
      |||
QY 596 GCCACTGCTCTGCTGCTGAGGTGAAGACCGTGGGCCCCGGTCAATGTCGGCTTCGGCT 655
      |||
Db 179 TCCCTTGSCCAGACATGCTGGAGTGCAGCGCTTTCGCCGAG-ACAACGACCTCTCATCC 237
      |||
QY 656 TCCCTTGSCCAGACATGCTGGAGTGCAGCGCTTTCGCCGAGCAACGACCTTCATCC 715
      |||
Db 238 CCCTCGCTAGTAG-GACCACCTCTCGCGGCACAGAGGAAGCTCCCAAGGTGTGTGAAG 296
      |||
QY 716 CCCTCGCTAGTAGGACACCTCTCGCGGCACAGAGGAAGCTCCCAAGGTGTGTGAAG 775
      |||
Db 297 CCTGCAAAACCAAGATGAGGACGACATCATGGAACCCCTTTGTAAAAATGACT 356
      |||
QY 776 CCTGCAAAATAAAAATGATGATGACAAACGATAATGGAACCGCTTTGTAAAAATGATT 835
      |||
Db 357 TCGCAGTGAATAAAGTGAAGGAGATAAGTACATCAACAGAGACACCAAGATCATCC 416
      |||
QY 836 TTGACCTGAAATAAAGTGAAGGAGATAAGTACATCAACGAGATACCAAAATCATCC 895
      |||
Db 417 TGGAGACAAAGACGACCACTTTACAAAGCTGAACGGCGTGT 458
      |||
QY 896 TGGAGACCAAGACGACCACTTTACAAAGCTGAACGGGTGT 937
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```

```
RESULT 22
LOCUS AA429960 378 bp mRNA EST 16-OCT-1997
DEFINITION zw58g10.r1 Soares total fetus Nb2HF8 9w Homo sapiens CDNA clone
774306 5', mRNA sequence.
ACCESSION AA429960
NID g2113134
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 378)
AUTHORS Hallier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
TITLE Contact: Wilson RK
JOURNAL Washington University School of Medicine
COMMENT 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
```

Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 352.

FEATURES

Location/Qualifiers
1. .378
/organism="Homo sapiens"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCTTAATTTTGTGTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone="774306"
/clone_lib="Soares total fetus Nb2HF8 9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
BASE COUNT 115 a 101 c 88 g 74 t
ORIGIN

Query Match 17.9%; Score 362; DB 10; Length 378;
Best Local Similarity 99.2%; Pred. No. 0.00e+00;
Matches 370; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Db 7 CCGGTCATGTCGCCCTTCG-CTTCCCTGGCCGACATGCTTGAGTGGACGCTTTCC 65
QY 633 CCGGTCATGTCGCCCTTCGCTTCCCTGGCCGACATGCTTGAGTGGACGCTTTCC 692
Db 66 CCAGGACACGACCTTTGGCATCCCTCGTAGCAGCACCCTCTGCGAGCCACCGA 125
QY 693 CCAGGACACGACCTTTGGCATCCCTCGTAGCAGCACCCTCTGCGAGCCACCGA 752
Db 126 GGNAGTCCAAAGGTATGTGAACCTTGCAAAATAAAATGATGATGACACGACATAAT 185
QY 753 GGAAGCTCCAAAGGTATGTGAAGCTTGCAAAATAAAATGATGATGACACGACATAAT 812
Db 186 GGAACGCTTTGTAATAATGATTTGCACGTGAAATAAAGTGAAGAGATAACCTACAT 245
QY 813 GGAACGCTTTGTAATAATGATTTGCACGTGAAATAAAGTGAAGAGATAACCTACAT 872
Db 246 CRAACGAGATACCAAAATCATCTCGGAGACCAAGACACCATTTACAGCTGAACGG 305
QY 873 CRAACGAGATACCAAAATCATCTCGGAGACCAAGACACCATTTACAGCTGAACGG 932
Db 306 TGTGTCGGAATAGGACCTGAAGAAATCGGTGCTGGCTCAAAAGACAGCTTGCAAGTGCAC 365
QY 933 TGTGTCGGAAGGACCTGAAGAAATCGGTGCTGGCTCAAAAGACAGCTTGCAAGTGCAC 992
Db 366 CTGTGGAGAGATG 378
QY 993 CTGTGGAGAGATG 1005

RESULT 23
LOCUS AA024772 433 bp mRNA EST 13-AUG-1996
DEFINITION ze76g10.s1 Soares fetal heart NBHH19W Homo sapiens cDNA clone
364962 3', mRNA sequence.
ACCESSION AA024772
NID g1489678
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 433)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hollman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)

TITLE

JOURNAL

COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. from Amersham
High quality sequence stop: 289.

FEATURES

source

1. .433
/organism="Homo sapiens"
/note="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTGTGTTT 3'].
Double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library was constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHL19W."
/db_xref="taxon:9606"
/clone="364962"
/clone_lib="Soares fetal heart NBHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
complement(<1..>433)
BASE COUNT 150 a 51 c 87 g 141 t 4 others
ORIGIN

Query Match 17.9%; Score 363; DB 23; Length 433;
Best Local Similarity 99.2%; Pred. No. 0.00e+00;
Matches 369; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Db 1 GTAAACAGGATGTAAAGTTTATACAAAGATATAATGTTTATCTGAAATATTACAGT 60
Cp 2000 GTAAACAGGATGTAAAGTTTATACAAAGATATAATGTTTATCTGAAATATTACAGT 1941
Db 61 GTTGGTTAAAGCAATATTTTACAACTTTTAAAGGTAACACTACTATGTATATTACAGTA 120
Cp 1940 GTTGGTTAAAGCAATATTTTACAACTTTTAAAGGTAACACTACTATGTATATTACAGTA 1881
Db 121 AGCTACAATGGGTTTAATTTGCAAAAGTTAAGTAAGAAATGTTTTAAACAAGGCTTAAAG 180
Cp 1880 AGCTACAATGGGTTTAATTTGCAAAAGTTAAGTAAGAAATGTTTTAAACAAGGCTTAAAG 1821
Db 181 TACTCAAGTCAATTAATAAATTTATATCTTTTGCTTTTACTTGAAGAAATCATGCTATA 240
Cp 1820 TACTCAAGTCAATTAATAAATTTATATCTTTTGCTTTTACTTGAAGAAATCATGCTATA 1761
Db 241 GAAATGGTTAATGCTTCTAATAAATGGAAGTATTGTAGCTGGAATGTGATACATGTAA 300
Cp 1760 GAAATGGTTAATGCTTCTAATAAATGGAAGTATTGTAGCTGGAATGTGATACATGTAA 1701
Db 301 CAGTTTAAGTCCCATTTGAAGGTATAAANTGATGAATTTGTTGAAGACTTAGACACNGGA 360
Cp 1700 CAGTTTAAGTCCCATTTGAAGGTATAAANTGATGAATTTGTTGAAGACTTAGACACCTG-A 1642
Db 361 GTCTCAGTCNGG 372
Cp 1641 GTCTCAGTCG 1630

RESULT 24
 LOCUS H87071 426 bp mRNA EST 21-NOV-1995
 DEFINITION YS74d07.r1 Homo sapiens cDNA clone 220525 5' similar to SP:A45054
 A45054 FZ-1-PUTATIVE INTERCELLULAR SIGNAL TRANSDUCER OR TRANSMITTER
 -
 ACCESSION H87071
 NID 91068650
 KEYWORDS EST.
 SOURCE human clone=220525 primer=M13RP1 library=Soares retina N2b4HR
 vector=ptT3D (Pharmacia) with a modified polylinker host=DH10B
 (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI 1st strand cDNA
 was primed with a Not I- oligo(dT) primer
 [5'-TGTTACCAATCTGAAGGGAGGCGCGCTTTTTTTTTTTTTTTT-3'],
 double-stranded cDNA was size selected, ligated to Eco RI adapters
 (Pharmacia), digested with Not I and cloned into the Not I and Eco
 RI sites of a modified pT73 vector (Pharmacia). The retinas were
 obtained from a 55 year old Caucasian male and total cellular
 poly(A)+ RNA was extracted 6 hrs after their removal. The retina
 RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the
 University of Toronto. Library constructed by Bento Soares and
 M. Fatima Bonaldo.
 ORGANISM Homo sapiens
 Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 426)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
 Holman, M., Hultman, M., Kuababa, T., Le, M., Lennon, G., Marra, M.,
 Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, F.,
 Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and
 Wilson, R.
 TITLE The WashU-Merck EST Project
 JOURNAL Unpublished (1995)
 COMMENT Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 High quality sequence stops: 355
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 FEATURES
 source Location/Qualifiers
 1..426
 /organism="Homo sapiens"
 /clone="220525"
 mRNA <1..>426
 BASE COUNT 96 a 128 c 110 g 83 t 9 others
 ORIGIN
 Query Match 17.7%; Score 359; DB 21; Length 426;
 Best Local Similarity 94.8%; Pred. No. 0.00e+00;
 Matches 399; Conservative 0; Mismatches 17; Indels 5; Gaps 5;
 Db 2 ACGGATGATGATACAGAACATCGCGCTGCCAACCTGCTGGGCCACGAGACCATGAAGG 61
 |||||
 Qy 407 ACGGATCGAATACAGAACATCGCGCTGCCAACCTGCTGGGCCACGAGACCATGAAGG 466
 |||||
 Db 62 AGGTGCTGGAGCGCGCGCTTGATGATCCCGCTGGTATGAGCAGTGCACCGGACA 121
 |||||
 Qy 467 AGGTGCTGGAGCGCGCGCTTGATGATCCCGCTGGTATGAGCAGTGCACCGGACA 526
 |||||
 Db 122 CAAGAAGTCTCTGTGCTGCTTTCGCGCCCGCTGCTGCTGATGACCTAGACGAGACA 181
 |||||
 Qy 527 CCAGAAGTCTCTGTGCTGCTTTCGCGCCCGCTGCTGCTGATGACCTAGACGAGACA 586
 |||||
 Db 182 TCCAGCCATGCCACTGCTGCTG-GTGCAAGGTGAAGACCGCTGCGCCCGCTGATGCTC 240

Qy 587 TCCAGCCATGCCACTCGCTCTCGTGCAGGTGAA-GGACCGTGCCTCCCGCTCATGTCC 645
 |||||
 Db 241 GCCTTCGGTTTCCCTGGCCCGACATGCTGTAGTGCAGCGTTTCCCGCAGACACGAC 300
 |||||
 Qy 646 GCCTTCGGCTTCCCTGGCCCGACATGCTGTAGTGCAGCGTTTCCCGCAGACACGAC 705
 |||||
 Db 301 CTTTGCATCCCTCTGNTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 350
 |||||
 Qy 706 CTTTGCATCCCTCTGNTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 764
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 Db 361 GGTATGTGAAGCTGNAATAATTAATAATGATGATGATGATGATGATGATGATGATGATGAT 420
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 Qy 765 GGTATGTGAAGCTGCAATAATTAATAATGATGATGATGATGATGATGATGATGATGATGAT 822
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 Db 421 T 421
 Qy 823 T 823
 RESULT 25
 LOCUS AA295018 359 bp mRNA EST 18-APR-1997
 DEFINITION EST100474 Pancreas tumor I Homo sapiens cDNA 5' end, mRNA sequence.
 ACCESSION AA295018
 NID 91947649
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryotes; mitochondria; eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae;
 Homo.
 REFERENCE 1 (bases 1 to 359)
 AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
 Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
 White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
 Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
 Fitzgerald, L.M., Fitch, W.M., Fritchman, J.L., Geoghegan, N.S.,
 Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
 Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmar, S.M., Merrick, J.M.,
 Moreno-Palances, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
 Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
 Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
 Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
 Dimke, D., Feng, D.-F., Ferris, A., Fischer, C., Hastings, G.A.,
 He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
 Kozak, D.L., Kunsch, C., Hung, J., Li, H., Weissner, P.S., Olsen, H.,
 Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
 Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
 Fraser, C.M. and Venter, J.C.
 TITLE Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
 MEDLINE 96026280
 COMMENT Other_ESTs: THCI80057
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.
 Location/Qualifiers
 1..359
 /organism="Homo sapiens"
 /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
 EcoRI; Site_2: XhoI"
 /db_xref="ATCC (inhost):190769"
 /db_xref="taxon:9606"
 /clone_lib="Pancreas tumor I"

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ORIGIN										
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Best Local Similarity	97.8%	Pred. No. 0.00e+00;								
Matches	351;	Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0;					
Db	1	CGTCAGGTGAAGACCGCTGCGCCCGGTCATGTCGGCCTTCGGNTTCCTCGCCCGCA	60							
QY	609	CGTCAGGTGAAGACCGCTGCGCCCGGTCATGTCGGCCTTCGGCTTCCTCGCCCGCA	668							
Db	61	CATGCTTGANTGACACNTTCCCGCAGGACACGACCTTTGACATCCCTTCGCTAGCAG	120							
QY	669	CATGCTTGAGTGCACGGTTCCTCCCGCAGGACACGACCTTTGACATCCCTTCGCTAGCAG	728							
Db	121	CGACCACTCTCTCCCGCAGGACCGGAGGAGCTCCAAAGGTATGTNAAGCTGCAGAAATAA	180							
QY	729	CGACCACTCTCTCCCGCAGGACCGGAGGAGCTCCAAAGGTATGTNAAGCTGCAGAAATAA	788							
Db	181	AAATGATGATGACACACATATGGAAGACCTTTGTAAATAATNATTTGACCTGAAAT	240							
QY	789	AAATGATGATGACACACATATGGAAGACCTTTGTAAATAATNATTTGACCTGAAAT	848							
Db	241	AAAAGTGAAGGAGATACCTACATCAACCGAGATACCAAAATATCTCTGGAGACCAAGAG	300							
QY	849	AAAAGTGAAGGAGATACCTACATCAACCGAGATACCAAAATATCTCTGGAGACCAAGAG	908							
Db	301	CAAGACATTTACAGCTGAACGGTGTGTCGGAAGGAGCTGAAGGAATCGGTGCTGT	359							
QY	909	CAAGACATTTACAGCTGAACGGTGTGTCGGAAGGAGCTGAAGGAATCGGTGCTGT	967							
RESULT	26	AT047549	449 bp	mRNA	EST	08-JUL-1998				
LOCUS										
DEFINITION	un80808.r1 Soares mouse urogenital ridge NMUR Mus musculus cDNA clone 1763991 5', similar to TR:008862 O08862 SECRETED FRIZZLED RELATED PROTEIN SRP-2. [2] TR:P97299 ;, mRNA sequence.									
ACCESSION	A1047549									
NID	g3295836									
KEYWORDS	EST.									
SOURCE	house mouse.									
ORGANISM	Mus musculus									
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.									
AUTHORS	1 (bases 1 to 449)									
	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilton,R. and Waterston,R.									
TITLE	The WashU-HMMI Mouse EST Project									
JOURNAL	Unpublished (1996)									
COMMENT	Contact: Marra M/Mouse EST Project WashU-HMMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:963515 Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 442. Location/Qualifiers 1. .449 /organism="Mus musculus" /note="Organ: gonad; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5']									
FEATURES										
source										

Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 406)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The Washu-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
High quality sequence stops: 321
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infoimage.llnl.gov) for further information.
FEATURES
Location/Qualifiers
1..406
/organism="Homo sapiens"
/clone="159560"
BASE COUNT 130 a 94 c 103 g 77 t 2 others
ORIGIN
Query Match 16.6%; Score 337; DB 20; Length 406;
Best Local Similarity 98.1%; Pred. No. 0.00e+00;
Matches 388; Conservative 0; Mismatches 2; Indels 5; Gaps 5;
Db 1 CCCAGGACACGACCTTTGTCATCCCTCGCTAGCAGCAGCACCCTCTGCGAGCCACCG 60
Qy 692 CCCAGGACACGACCTTTGTCATCCCTCGCTAGCAGCAGCACCCTCTGCGAGCCACCG 751
Db 61 AGGAAGCTCCAAAGTATGTGAAGCTCCAAATATAAATATGATGATGACACGACATAA 120
Qy 752 AGGAAGCTCCAAAGTATGTGAAGCTCCAAATATAAATATGATGATGACACGACATAA 811
Db 121 TGGAAACCTTTTGAATAATGATTTTGACCTGAAATATAAAGTGAAGGAGATACTTACA 180
Qy 812 TGGAAACCTTTTGAATAATGATTTTGACCTGAAATATAAAGTGAAGGAGATACTTACA 871
Db 181 TCAACCGAGATACCAAAATATCTCTGGAGACCAAGACCAACATTTTCAAGCTGAACG 240
Qy 872 TCAACCGAGATACCAAAATATCTCTGGAGACCAAGACCAACATTTTCAAGCTGAACG 931
Db 241 GTGTGTCGGAAGGACCTGAAGAAATCGGTGCTGCTGCTCAAGACAGCTTGCAAGTCA 300
Qy 932 GTGTGTCGGAAGGACCTGAAGAAATCGGTGCTGCTGCTCAAGACAGCTTGCAAGTCA 991
Db 301 CCTGTGAGGAGATCAACACATCAACCGCCCTATCTGTTTCATGGGAGGAGAAACAG 360
Qy 992 CCTGTGAGGAGATCAACACATCAACCGCCCTATCTGTTTCATGGGAGGAGAAACAG 1047
Db 361 GGTGGGAGCTGGT 375
Qy 1048 GGT-GGGGAGCTGGT 1061
RESULT 28
LOCUS HUM296B07B 340 bp mRNA EST 21-MAY-1996
DEFINITION Human aorta cDNA 5'-end GEN-296B07, mRNA sequence.
ACCESSION D62525
NID 9866299
KEYWORDS EST; EST(expressed sequence tag); Human aorta; similar to none(May 29,1995).
SOURCE Homo sapiens cDNA to mRNA, clone_lib:Clontech human aorta polyA+ mRNA (#6572).
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae;

Homo.
1 (bases 1 to 340)
Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M.,
Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H.,
Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y.,
Maekawa, H., Shin, S. and Nakamura, Y.
Unpublished (2003)
Unpublished (1995)
2 (bases 1 to 340)
Fujiwara, T.
Direct Submission
Submitted (30-MAY-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu
Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical
Co., Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
Japan (Tel:0886-65-2888, Fax:0886-37-1035)
Submitted (30-May-1995) to DDBJ by:
Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 Kagasuno Kawauchi-cho
Tokushima, Tokushima
771-01
Japan
Phone: 0886-65-2888
Fax : 0886-37-1035.
Location/Qualifiers
1..340
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Clontech human aorta polyA+ mRNA (#6572)"
BASE COUNT 113 a 64 c 38 g 122 t 3 others
ORIGIN
Query Match 16.3%; Score 331; DB 6; Length 340;
Best Local Similarity 98.5%; Pred. No. 0.00e+00;
Matches 335; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
Db 1 CATCTTCATCAGCTCCAGACTGAGACTCAGTGTCTTAAGTCTTACACAAATTCATCATTTT 60
Qy 1616 CATCTTCATCAGCTCCAGACTGAGACTCAGTGTCTTAAGTCTTACACAAATTCATCATTTT 1675
Db 61 ATACCTTCAATGGGAACTTAACTGTATCATGTATCATCCAGCTACATATCTCCAT 120
Qy 1676 ATACCTTCAATGGGAACTTAACTGTATCATGTATCATCCAGCTACATATCTCCAT 1735
Db 121 TTATTAGAGGACATTAACCAATTTCTATAGCATGATTTCTTCAAGTAAAGGCAAAAGAT 180
Qy 1736 TTATTAGAGGACATTAACCAATTTCTATAGCATGATTTCTTCAAGTAAAGGCAAAAGAT 1795
Db 181 ATAAATTTTATAATGACTTGAGTACTTTAAGCCCTGTTTAAACATTTCTTACTTAAC 240
Qy 1796 ATAAATTTTATAATGACTTGAGTACTTTAAGCCCTGTTTAAACATTTCTTACTTAAC 1855
Db 241 TTTGGCAATTAACCCATTTAGCTTACCTGTAATATACATAGTGTGTACCTTTAA 300
Qy 1856 TTTG-CAAAATTAACCCATTTAGCTTACCTGTAATATACATAGTGTGTACCTTTAA 1914
Db 301 GTTGTAATAATATGCTTTTACCAACACTGTAATAATTTTC 340
Qy 1915 GTTGTAATAATATGCTTTTACCAACACTGTAATAATTTTC 1954
RESULT 29
LOCUS AA073862 396 bp mRNA EST 15-FEB-1997
DEFINITION mm97f07.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone
536389 5' similar to TR:G1151260 G1151260 TRANSMEMBRANE RECEPTOR.
; mRNA sequence.
ACCESSION AA073862
NID g1595602
KEYWORDS EST.
SOURCE House mouse.
ORGANISM Mus musculus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 396)
 AUTHORS Marra,M., Haller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucnba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Willson,R. and Waterston,R.

TITLE The WashU-HMMI Mouse EST Project
 COMMENT Unpublished (1996)

Contact: Marra M/Mouse EST Project
 WashU-HMMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:323325
 Seq primer: -28ml3 rev1 ET from Amersham
 High quality sequence stop: 390.
 Location/Qualifiers
 1. .396
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 /strain="NIH/Swiss"
 /note="vector: phluescript SK-; Site.1: EcoRI; Site.2: XhoI; Cloned unidirectionally. Primer: Oligo dt. 93 pooled NIH/Swiss 13 day embryo hearts. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor sequence: 5' CTCGAGTGTGTGTGTGTGTGTGT 3'"
 /db_xref="taxon:10090"
 /clone="536389"
 /clone_lib="Stratagene mouse heart (#937316)"
 /sex="pooled"
 /dev_stage="13 day embryos"
 /lab_host="SOLR (kanamycin resistant)"
 <1. .>396

BASE COUNT	93 a	126 c	103 g	74 t
ORIGIN				

Query Match 16.2%; Score 328; DB 26; Length 396;
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 Matches 368; Conservative 0; Mismatches 28; Indels 2; Gaps 2;

Db	1	AGCAGGCGGGCGCT-GGATTCGGTGTGTCATGAAGCAGTGCACCCGACACCAAGAGT	59
QY	476	AGCAGGCGGGCGCTGGAGTCCCGTGTGTCATGAAGCAGTGCACCCGACACCAAGAGT	535
Db	60	TCCTGTGCTCCTCTTCGCCCTCTGCTCTCTCGAGGACCTAGATCAGACCATCCAGCCGT	119
QY	536	TCCTGTGCTCCTCTTCGCCCTCTGCTCTCGATGACCTAGACGAGACCATCCAGCCAT	595
Db	120	GTCACCTCGCTCTG-GTGCAGGTGAAGGACCGCTGCCGCCGCTATGTCGGCTTCGGCT	178
QY	596	GCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCCGCCGCTATGTCGGCTTCGGCT	655
Db	179	TCCCTGCGCCAGACATGCTGGAGTGCAGACGTTTCCCGCAGAGCAACGACCTCTCGATCC	238
QY	656	TCCCTGCGCCGACATGCTTGAGTGCAGACGTTTCCCGCAGAGCAACGACCTTTCATCC	715
Db	239	CCCTCGCTAGTAGGACCACTCTCTGCCGCCACAGAGAGGACTCCCAAGGTGTCTGAAG	298
QY	716	CCCTCGCTAGCAGGACCACTCTCTGCCGCCACGAGAGGACTCCCAAGGTGTCTGAAG	775
Db	299	CCTGCAAAACCAAGAAATGAGGACGACACGACATCATGGAACCCCTTTGTAATAAATGACT	358
QY	776	CCTGCAAAATAAATAATGATGATGACACAGACATAATGGAACGCTTTGTAATAAATGATT	835
Db	359	TCCGACTGAAATCAAAGTGAAGGAGATAACGTATCATC	396

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QY 626 GCTGCGCCCGGTCATGTCGCTTCGGCTTCCTCCCTGGCCG-ACATGCTTGAGTGGAC 684
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QY 685 CGTTTCCCCAGACACGACCTTTGATCCTCCCTCGCTAGCAGCACCACCTTCCTGCCA 744
Db 241 GCACCCGAGAGCTCCAAAGGTATCTGAGCCTGCAAGATTAATAAATGATGATGACAC 300
QY 745 GCCACGAGGAGCTCCAAAGGTATCTGAGCCTGCAAGATTAATAAATGATGATGACAC 804
Db 301 GACATTAATGGAACGCTTTGTAATAATGATTTTGCACCTGAAAATTTNAAAGTGAAGGA 360
QY 805 GACAT-AATGGAACGCTTTGTAATAATGATTTTGCACCT-GAAAAATGATGATGACAC 860
Db 361 GATAACCT 368
QY 861 GATAACCT 868

RESULT 31
LOCUS AA705737 329 bp mRNA EST 24-DEC-1997
DEFINITION zf41b02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone
379467 3', mRNA sequence.
ACCESSION AA705737
NID 92715655
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 329)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 319.
FEATURES
Location/Qualifiers
1..329
/organism="Homo sapiens"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TCTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NbHL19W."
/db_xref="GDB:1287723"
/db_xref="taxon:9606"
/clone="379467"
/collection="Soares fetal heart NbHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
120 a 32 c 59 g 118 t

BASE COUNT
ORIGIN

```

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Query Match 15.98; Score 323; DB 12; Length 329;
Best Local Similarity 99.18; Pred. No. 0.00e+00;
Matches 326; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 1 TTTAGGTTAAACAGGAGTGTAAAGTTTATATACAAAGATAATAATGTTTATCTGAAATATTT 60
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Cp 2005 TTTAGGTTAAACAGGAGTGTAAAGTTTATATACAAAGATAATAATGTTTATCTGAAATATTT 1946
|||||
Db 61 ACAGTGTGGTTAAAGCAATATTTTACAACTTTTAAAGGTTAAAGTAACTACTATGTATATATAC 120
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Cp 1945 ACAGTGTGGTTAAAGCAATATTTTACAACTTTTAAAGGTTAAAGTAACTACTATGTATATATAC 1886
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Db 121 AGTAACTACAACTGGGTTTAAATTCGAAAAGTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 180
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Cp 1885 AGTAACTACAACTGGGTTTAAATTCGAAAAGTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 1826
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Db 181 TAAAGTACTCAAGTCAATTAATAAATTTATATCTTTTGGCTTTTACTTGGAGAGTTCATG 240
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Cp 1825 TAAAGTACTCAAGTCAATTAATAAATTTATATCTTTTGGCTTTTACTTGGAGAGTTCATG 1766
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|||||
Cp 1765 CTATAGAGATGGTTAAATGTCTTCTTAATAAGGAAGTATTTAGCTGGAATGTGATACA 1706
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Db 301 TGTAAACAGTTTAAAGTTCCTCCATTCGAAGTA 329
|||||
Cp 1705 TGTAAACAGTTTAAAGTTCCTCCATTCGAAGTA 1677
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RESULT 32
LOCUS H44092 434 bp mRNA EST 31-JUL-1995
DEFINITION Y073a07.r1 Homo sapiens cDNA clone 183540 5'.
ACCESSION H44092
NID 9920144
KEYWORDS EST.
SOURCE human clone-183540 library-Soares breast 3NBHbSt vector-pT7T3D
(Pharmacia) with a modified polylinker host-DH10B (ampicillin
resistant) primer-M13RP1 Rsite1-Not I Rsite2-Eco RI Adult human.
1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia),
digested with Not I and cloned into the Not I and Eco RI sites of a
modified pT7T3 vector (Pharmacia). Library went through one round
of normalization to a Cot = 20. Library constructed by Bento Soares
and M.Fatima Bonaldo.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 434)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rafkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 123
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
Location/Qualifiers
1..434
/organism="Homo sapiens"
source

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TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)

Clodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P. S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palmerques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Springs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D. F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hwangjun, J., Li, H., Meisner, P. S., Olsen, H., Raymond, L., Wei, Y. F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillion, P. J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)

96026280
 Order# 0347 Supp# 1, 3 174 (1992)
 Other_ESRs: THC180057
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423

Email: alexzavetigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tadb/hgi/hgi.html>)
Seq primer: M13 Reverse.

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FEATURES
source
seq primer: fwd reverse
Location/Qualifiers
1..328
/organism="Homo sapiens"
/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
/db_xref="ATCC (inhost):191138"
/db_xref="taxon:9606"
/clone_lib="Pancreas tumor I"
/dev_stage="adult"
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mRNA

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Query Match	15.8%	Score 320;	DB 4;	Length 328;
Best Local Similarity	99.4%;	Pred. No. 0.00e+00;		
Matches 326;	Conservative 0;	Mismatches 1;	Indels 1;	Gaps 1;
Db	1	CCTAGCTGCTCCAGTCFCACGCTGGGCGAGCTCCCCCTGCCTTTTTCGACGTTTGCAATCCC	60	
Qy	1236	CCTAGCTGCTCCAGTCFCACGCTGGGCGAGCTCCCCCTGCCTTTTTCGACGTTTGCAATCCC	1295	
Db	61	CAGCATTTCTCTGAGTTATAAGGCCACAGGAGTGGATAGCTGTTTTTCCACCTAAAGGAAAG	120	
Qy	1296	CAGCATTTCTCTGAGTTATAAGGCCACAGGAGTGGATAGCTGTTTTTCCACCTAAAGGAAAG	1355	
Db	121	NCCACCGCAATCTTGTAGAAATATTTCAAACATAATAATCATGAATATTTTTTATGAAGTT	180	
Qy	1356	CCCACCGCAATCTTGTAGAAATATTTCAAACATAATAATCATGAATATTTTTTATGAAGTT	1415	
Db	181	TAAAAATAGCTCACTTTTAAAGCTAGTTTTTCAATAGGTGCNACTGTGACITGGGCTCGGTT	240	
Qy	1416	TAAAAATAGCTCACTTTTAAAGCTAGTTTTTCAATAGGTGCNACTGTGACITGGGCTCGGTT	1475	
Db	241	GGTTGTTGTTGTTGTTTTCGAGTCAGCTGATTTTTCACCTCCCACTGAGGTTGTGCATAAACA	300	
Qy	1476	GGTTGTTGTTGTTGTTTTCGAGTCAGCTGATTTTTCACCTCCCACTGAGGTTGTGCATAAACA	1535	
Db	301	TGCAAAATGCTTCAATTTTTTCTCTGCGG	328	
Qy	1536	TGCAAAATGCTTCAATTTTTTCTCTGCGG	1562	

RESULT	35				
LOCUS		HI5818	469 bp	mRNA	EST
DEFINITION		y128c05.s1 Homo sapiens cDNA clone 159560 3'.			

ACCESSION
NID
KEYWORDS
SOURCE

human clone-19560 library-Soares breast 3NtBst vector-pv7T3D (Pharmacia) with a modified polynuker host-DH10 (ampicillin resistant) primer-Promega -21m31 Raitel-Not I Raites-Eco RI Adult human 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGCCGCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pv7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fátima Bonaldó

ORGANISM

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
AUTHORS

BARRERA, ALONSO; FERRERES, CATALINA; ROMILLODE, ROMO.
1 (bases 1 to 469)
Hillier L., Clark N., Dubuque T., Ellison K., Hawkins M.,
Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
Trevasaki E., Waterston R., Williamson A., Wohlmann P. and
Wilson R.

TITLE	COMMENT
The WashU-Merck EST Project Unpublished (1995)	

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Fax: 314 280 1810
Email: est@watson.wustl.edu
High quality sequence stons: 340

high quality sequence stops: 340
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
SOURCE

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1.403
/organism="Homo sapiens"
/clone="159560"

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BASE COUNT	144 a	65 c	106 g	150 t	4 others
ORIGIN					

Query Match	15.8%	Score 321;	DB 20;	Length 469;
Best Local Similarity	97.1%;	Prod NC	0.00e+00.	

Best Local Similarity 97.1%; Pred. NO. 0.00e+00;
Matches 370; Conservative 0; Mismatches 3; Indels 8; Gaps 8;

Db 1 AGGTAAACAGGATTAAAGTTTATATACAAGAAATATAATGTTTATCTGAAATAATTACA 60

22 1 AGGAGGATTCACAGATTTTAAAGGTTTTATATACAGAGGATTAATAGTGTATATCTCGAATAATATACA
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Cp		2002	AGGATATTACAGGATGTAAGAATTTTAAATATACAGGAATAAATGGTTTTATCTCGAATAATATTTACA	194
Dp	61	GTCGTGGGTTAAAGCAATATTTTACAACATTTTAAAGCTAAACTACTATCTATATTACAGG		120

D9	G G G G T G G T T A A G C C A T A T T T T A C A C C T T T A A A G G T A T A C A G G A T A T T A C A G G
Cp	G T G T G G T T A A G C C A T A T T T T A C A C C T T T A A A G G T A T A C A G G A T A T T A C A G G

[illegible]

DD	121	TTAGGCTACATGGGGTCTTAAATTTGCAAAAGGTTAAGTAAAGAAATATGTTTTTAAACACAGGCTTAA	180
Cp	1882	TAAGTACATGGGGTCTTAAATTTGCAAAAGGTTAAGTAAAGAAATATGTTTTTAAACACAGGCTTAA	1823

1002	TAAGGTCACAAAGGGGTTTAAATTTTCATTAAGTAAGGAAATAGTTTTTAATACAAAGGCTTAA	1022
Cp		
181	AGTACTCAAGTCAATATATAAATTATATCTTTTGGCTTTTACTTGAAGAAATCATGCTA	240
Dp		

D5
AGATGCGACGGCCTCAATTATAAAATTTTAAATCTTTTTTGCCCTTTTACCTTTGAAGAAAATCATGCCTA 240

Cp
1822 AGTACTCAGTCGAATTAATAAAATTTTATATCTTTTGGCTTTTCTTGTGAGAAATCATGCTCA 1763

CP 1022 AGTACCTCAGGCGCAATATATATATATATATATATCTCTTTGGCTTTTACCTTGAAGATATACAGTCA 178

Db 241 TAGAATGGTTAATGTGCTTCTCTAATAAATGGGCAAGCATTTGAGCTGGGAAATGTGATACA 300

25
241
Cp

db 301 TGT AAC AGT TTA AGG TTCC CCA TGA AGG GTATA AAT GAT GAAT TCT CTCTA AGG NCTTAG 360
cf 1702 TAG AAA TGG TTT AAG TGG TGG TGC CTC AAT AAA TGG 1709 AAG CAT TGG TAG CTGG AAT GGGA TACA 1709

[illegible][illegible]

[illegible]

Db	121	CATAACATGCAAAATGCTTCAATTTCTCTGTGGCCCAAACTTGTGGGTACAAACCCGTG	180
QY	1529	CATAACATGCAAAATGCTTCAATTTCTCTGTGGCCCAAACTTGTGGGTACAAACCCGTG	1598
Db	181	TTGAGATAAGCTGGCTGTTATCTCAACATCTTCAATCAGCTCCAGACTGAGACATCAGTGT	240
QY	1589	TTGAGATAAGCTGGCTGTTATCTCAACATCTTCAATCAGCTCCAGACTGAGACATCAGTGT	1648
Db	241	CTAAGTCTTTACAAACAATTCATCATTTTATACCTTCAATGGGAACCTTAAACTGGTTCCAT	300
QY	1649	CTAAGTCTTTACAAACAATTCATCATTTTATACCTTCAATGGGAACCTTAAACTGGTTCCAT	1706
Db	301	GTATCACAATCCAGCTACAATCAATCTCCATTTAAATTAGANGCAC	344
QY	1707	GTATCACA-TTCAGCTACAATCAATCTCCATTTA-TTGAAGCAC	1748
RESULT	39		
LOCUS	HUM303B01B	301 bp	mrna
DEFINITION	Human aorta cDNA 5'-end	GEN=303B01,	EST
ACCESSION	D79675		14-DEC-1995
NID	g1180026		
KEYWORDS	EST; EST(expressed sequence tag); Human aorta.		
SOURCE	Homo sapiens aorta cDNA to mRNA, clone_lib:human aorta polyA+.		
ORGANISM	Homo sapiens		
	Eukaryotes; mitochondrionl eukaryotes; Metazoa; Chordata;		
	Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;		
	Homo,		
REFERENCE	1 (bases 1 to 301)		
AUTHORS	Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, K., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H., Shin, S. and Nakamura, Y.		
TITLE	Large-scale sequencing project at Otsuka GEN Research Institute		
REFERENCE	Unpublished (1995)		
AUTHORS	2 (bases 1 to 301)		
TITLE	Fujiwara, T.		
JOURNAL	Direct Submission		
TITLE	Submitted (07-NOV-1995) to the DDBJ/EMBL/GenBank databases. Tsuboi, T.		
JOURNAL	Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd, 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771 Japan		

```

Submitted (7-Nov-1995) to DDBJ by:
Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical CO.,Ltd
463-10 Kagasuno Kawauchi-cho
Tokushima, Tokushima
771-01
Japan
Phone:0886-65-2888
Fax :0886-37-1035,
FEATURES             Location/Qualifiers
     source           1..301
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone_lib="human aorta polyA+"
                        /tissue_type="aorta"
BASE COUNT           106 a    51 c    29 g    115 t
ORIGIN
Query Match          14.8%; Score 299; DB 6; Length 301;
Best Local Similarity 99.7%; Pred. No. 0.00e+00;
Matches 300; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 TACATGTATCACATTCCAGCTACAATACTTCCCATTTATTAGAAGCACATTAAACATTTC 60
      |||
QY 1702 TACATGTATCACATTCCAGCTACAATACTTCCCATTTATTAGAAGCACATTAAACATTTC 1761
      |||

Db 61 ATAGCATGATTTCTTCAAGTAAAGGCAAAAGATATAAAATTTTATAATTGACTTGGAGTAC 120
      |||
QY 1762 ATAGCATGATTTCTTCAAGTAAAGGCAAAAGATATAAAATTTTATAATTGACTTGGAGTAC 1821
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Db 1 CTGAGACTCAGTGTCTAAGTCTTTACAACAATTCATCAATTTTATACCTTCAATGGGAACCTT 60
 QY 1635 CTGAGACTCAGTGTCTAAGTCTTTACAACAATTCATCAATTTTATACCTTCAATGGGAACCTT 1694
 Db 61 AAAGTGTACATGTATACATTCCTCAGCTACATACCTTCCATTTATAGAGGCACATTAAC 120
 QY 1695 AAAGTGTACATGTATACATTCCTCAGCTACATACCTTCCATTTATAGAGGCACATTAAC 1754
 Db 121 CATTTCTATAGCATGATTTCTTCAAGTAAAGGCAAAAGATATAAATTTTATAATTGACT 180
 QY 1755 CATTTCTATAGCATGATTTCTTCAAGTAAAGGCAAAAGATATAAATTTTATAATTGACT 1814
 Db 181 TGAGTACTTTAAGCCCTGTTTAAACATTTCTTACTTAACCTTTTGCAA-TTAM-CCCAT 238
 QY 1815 TGAGTACTTTAAGCCCTGTTTAAACATTTCTTACTTAACCTTTTGCAAATTAACCCAT 1874
 Db 239 GTAGCTTACCTGTAATATACATAGTAGTTACCTTTAAARVGTGTAAATAATTTKCTTTA 298
 QY 1875 GTAGCTTACCTGTAATATACATAGTAGTTACCTTTAAAGTGTGAAAAATATTGCTTTA 1934
 Db 299 MCCAACACTGTAAT 313
 QY 1935 ACCAACACTGTAAT 1949

RESULT 42 HUM347H05B 303 bp mRNA EST 21-MAY-1996
 LOCUS
 DEFINITION Human aorta cDNA 5'-end GEN-347H05, mRNA sequence.
 ACCESSION D62999
 NID g966773

KEYWORDS EST: EST(expressed sequence tag); Human aorta; similar to none(May 29,1995).

SOURCE Homo sapiens cDNA to mRNA, clone_lib:Clontech human aorta polyA+ mRNA (#6572).

ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
 Homo.

REFERENCE 1 (bases 1 to 303)
 AUTHORS Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y., Maekawa,H., Shin,S. and Nakamura,Y.
 Unpublished(303)

JOURNAL Unpublished(1995)

REFERENCE 2 (bases 1 to 303)

AUTHORS Fujiwara,T.

TITLE Direct Submission

JOURNAL Submitted (30-MAY-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:0886-65-2888, Fax:0886-37-1035)

COMMENT Submitted (30-May-1995) to DDBJ by:

Tsutomu Fujiwara

Otsuka GEN Research Institute

Otsuka Pharmaceutical Co.,Ltd

463-10 Kagasuno Kawauchi-cho

Tokushima, Tokushima

771-01

Japan

Phone: 0886-65-2888

Fax : 0886-37-1035.

FEATURES

source

1. .303

Location/Qualifiers

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Clontech human aorta polyA+ mRNA (#6572)"

BASE COUNT 105 a 52 c 32 g 111 t

ORIGIN

Query Match 14.7%; Score 298; DB 6; Length 303;

Best Local Similarity 99.0%; Pred.No. 0.00e+00;

Matches 297; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 4 ACTCAGTCTCTAAGTCTTTACACAAATTCATCAATTTTATACCTTCAATGGGAACCTTAAACT 63
 QY 1640 ACTCAGTCTCTAAGTCTTTACACAAATTCATCAATTTTATACCTTCAATGGGAACCTTAAACT 1699
 Db 64 GTTACATGTATCACATTCAGCTACAAATCTCCATTTATAGAGGCACATTAACCATTT 123
 QY 1700 GTTACATGTATCACATTCAGCTACAAATCTCCATTTATAGAGGCACATTAACCATTT 1759
 Db 124 CTATAGCATGATTTCTTCAAGTAAAGGCAAAAGATATAAATTTTATATGACTTGA 183
 QY 1760 CTATAGCATGATTTCTTCAAGTAAAGGCAAAAGATATAAATTTTATATGACTTGA 1819
 Db 184 ACTTTAAGCCCTGTTTAAACATTTCTTACTTAACCTTTTGCAAATTAACCCATTTG 243
 QY 1820 ACTTTAAGCCCTGTTTAAACATTTCTTACTTAACCTTTTGCAAATTAACCCATTTG 1879
 Db 244 TTACCTGTAATATACATAGTAGTTACCTTTAAAGTGTGAAAAATATTGCTTTAACCAA 303
 QY 1880 TTACCTGTAATATACATAGTAGTTACCTTTAAAGTGTGAAAAATATTGCTTTAACCAA 1939

RESULT 43 AA347786 300 bp mRNA EST 21-APR-1997
 LOCUS
 DEFINITION EST54420 Fetal heart II Homo sapiens cDNA 3' end, mRNA sequence.
 ACCESSION AA347786

NID g2000261

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;

Homo.

REFERENCE 1 (bases 1 to 300)

AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulgner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Cocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palacios,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Weil,F.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (5547 Suppl), 3-174 (1995)

MEDLINE 96026280

COMMENT Other_ESTs: EST113252 THC180057

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tadb/hgi/hgi.html>)

Seq primer: M13-21.

Location/Qualifiers

1. .300

/organism="Homo sapiens"

/note="Organ: heart; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

/db_xref="ATCC (inhost):149068"

FEATURES

source

1. .300

/organism="Homo sapiens"

/note="Organ: heart; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

/db_xref="ATCC (inhost):149068"

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/db_xref="taxon:9606"
/clone_lib="Fetal heart II"
/dev_stage="fetus"
complement(<1..>300)
BASE COUNT      113 a      28 c      51 g      104 t      4 others
ORIGIN

Query Match      14.5%; Score 296; DB 4; Length 300;
Best Local Similarity 98.7%; Pred. No. 0.00e+00;
Matches 296; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1 AGTAAACAGGATGTAAGTTTATATACAAAGATATAATGTTTATCTGAAATATTACA 60
|||||
Cp 2002 AGTAAACAGGATGTAAGTTTATATACAAAGATATAATGTTTATCTGAAATATTACA 1943
|||||
Db 61 GTGTTGGTTAAAGCAATATTTTACAACTTTTAAAGGNAACACTATGATGATATACAG 120
|||||
Cp 1942 GTGTTGGTTAAAGCAATATTTTACAACTTTTAAAGGNAACACTATGATGATATACAG 1883
|||||
Db 121 TAAGCTACAAATGGTTTAAATTCGAAAGTTAAAGTAAGANATGTTTAAACAGGCTTAA 180
|||||
Cp 1882 TAAGCTACAAATGGTTTAAATTCGAAAGTTAAAGTAAGANATGTTTAAACAGGCTTAA 1823
|||||
Db 181 AGTACTCAAGTCAATATATAATTTTATCTTTGCGCTTTTACTTGAAGAAATCATGCTA 240
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Cp 1822 AGTACTCAAGTCAATATATAATTTTATCTTTGCGCTTTTACTTGAAGAAATCATGCTA 1763
|||||
Db 241 TAGAAATGGTTAATGCGTCTCTAATAAATGGAAGTATGTTAGCTGGAATGTGATACATGT 300
|||||
Cp 1762 TAGAAATGGTTAATGCGTCTCTAATAAATGGAAGTATGTTAGCTGGAATGTGATACATGT 1703
|||||

RESULT 44
LOCUS HUM307G04B 300 bp mRNA EST 21-MAY-1996
DEFINITION Human aorta cdna 5'-end GEN-307G04, mRNA sequence.
ACCESSION D62523
NID 9966397
KEYWORDS EST; EST(expressed sequence tag); Human aorta; similar to none(May 29,1995).
SOURCE Homo sapiens cdna to mRNA, clone_lib:Clontech human aorta polyA+ mRNA (#572).
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
Homo.
REFERENCE 1 (bases 1 to 300)
AUTHORS Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takaichi,A., Takeda S., Watanabe,T., Takahashi,E., Hirai,Y., Maekawa,H., Shin,S. and Nakamura,Y.
Unpublished(303)
REFERENCE 2 (bases 1 to 300)
AUTHORS Fujiwara,T.
Direct Submission
Submitted (30-MAY-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical Co.,Ltd. 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan (Tel:0886-65-2888, Fax:0886-37-1035)
Submitted (30-May-1995) to DDBJ by: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 Kagasuno Kawauchi-cho
Tokushima, Tokushima
771-01
Japan
Phone: 0886-65-2888
Fax : 0886-37-1035.
Location/Qualifiers
1. 300
/organism="Homo sapiens"
/db_xref="taxon:9606"

FEATURES
Source

/db_xref="taxon:9606"
/clone_lib="Clontech human aorta polyA+ mRNA (#572)"
BASE COUNT      107 a      51 c      28 g      113 t      1 others
ORIGIN

Query Match      14.5%; Score 294; DB 6; Length 300;
Best Local Similarity 99.3%; Pred. No. 0.00e+00;
Matches 299; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Db 1 TACAWGTATCACATTCAGCTACATCTCCATCTTATTAGACACATTAACCATTTCT 60
|||||
Cp 1702 TACATGTATCACATTCAGCTACATCTCCATCTTATTAGACACATTAACCATTTCT 1761
|||||
Db 61 ATAGCATGATTTCTCAAGTAAAGGCAAGATATAAATTTTATTAATGACTTGAGTAC 120
|||||
Cp 1762 ATAGCATGATTTCTCAAGTAAAGGCAAGATATAAATTTTATTAATGACTTGAGTAC 1821
|||||
Db 121 TTTAAGCCTTGTTTAAACATTTCTTACTTAACCTTTTGCATTAATTAACCCCATTTGAGTT 180
|||||
Cp 1822 TTTAAGCCTTGTTTAAACATTTCTTACTTAACCTTTTGCATTAATTAACCCCATTTGAGTT 1881
|||||
Db 181 ACCTGTAATATACATAGTAGTTTACCTT-AAAGTTTGTAAATATATTGCTTTAACCAACA 239
|||||
Cp 1882 ACCTGTAATATACATAGTAGTTTACCTT-AAAGTTTGTAAATATATTGCTTTAACCAACA 1941
|||||
Db 240 CTGTAATATTTTACAGATAACATATATCTTGTATATATAACTTTTACATCTGTTTACC 299
|||||
Cp 1942 CTGTAATATTTTACAGATAACATATATCTTGTATATATAACTTTTACATCTGTTTACC 2001
|||||
Db 300 T 300
Cp 2002 T 2002

RESULT 45
LOCUS AA330758 302 bp mRNA EST 21-APR-1997
DEFINITION EST34493 Embryo, 6 week I Homo sapiens cdna 5' end, mRNA sequence.
ACCESSION AA330758
NID 91983000
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
Homo.
REFERENCE 1 (bases 1 to 302)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-ai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wel,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cdna sequence
Nature 377 (6547 Suppl), 3-174 (1995)
JOURNAL 96026280
MEDLINE Other_ESTs: THCI80057
COMMENT Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423

```

Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tadb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers

1..302
/organism="Homo sapiens"
/note="Organ: embryo; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
/db_xref="ATCC (inhost):132379"
/db_xref="taxon:9606"
/clone_lib="Embryo, 6 week I"
/dev_stages="embryo, 6 wks"
<1..>302

BASE COUNT 99 a 57 c 82 g 56 t 8 others

ORIGIN

Query Match 14.4%; Score 292; DB 4; Length 302;
Best Local Similarity 97.0%; Pred. No. 0.00e+00;
Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 AACGACATAATGGAACCGCTTTGTAATAATNATTTNCACTGAAATAAAAGCTGAAGGAG 60
|||||
Qy 802 AACGACATAATGGAACCGCTTTGTAATAATNATTTNCACTGAAATAAAAGCTGAAGGAG 861
|||||
Db 61 ATAACCTACATCAACCGGAGATACCAAAATCATCTGGAGACCAAGCAAGACNNTTAC 120
|||||
Qy 862 ATAACCTACATCAACCGGAGATACCAAAATCATCTGGAGACCAAGCAAGACCATTTAC 921
|||||
Db 121 AAGCTGAACGCTGTCTCGAAGGACCTGAAGAATCGGTGCTGCTCAAGACAGC 180
|||||
Qy 922 AAGCTGAACGCTGTCTCGAAGGACCTGAAGAATCGGTGCTGCTCAAGACAGC 981
|||||
Db 181 TTGCAGTCACCTNNAGGAGATGAACGACATCAACGNGCCCTATCTGTCATGGGACAG 240
|||||
Qy 982 TTGCAGTCACCTGTGGAGAGATGAACGACATCAACGCGCCCTATCTGTCATGGGACAG 1041
|||||
Db 241 AANACGGGTGGGAGCTGGTGATCACCTCGGTGAAGCGGTGGCAGAGGGGCGAGAGAG 300
|||||
Qy 1042 AANACGGGTGGGAGCTGGTGATCACCTCGGTGAAGCGGTGGCAGAGGGGCGAGAGAG 1101
|||||
Db 301 TT 302
Qy 1102 TT 1103

RESULT 46 HUM238C04B 293 bp mRNA EST 21-MAY-1996
LOCUS Human aorta cDNA 5'-end GEN-238C04, mRNA sequence.
DEFINITION
ACCESSION D62097
NID 9965873
KEYWORDS EST; EST(expressed sequence tag); Human aorta; similar to none(May 29, 1995).
SOURCE Homo sapiens cDNA to mRNA, clone_lib:Clontech human aorta polyA+ mRNA (#6572).
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
Homo.
REFERENCE 1 (bases 1 to 293)
AUTHORS Fujiwara.T., Hirano.H., Katagiri.T., Kawai.A., Kuga.Y., Nagata.M., Okuno.S., Ozaki.K., Shimizu.F., Shimada.Y., Shinomiya.H., Takaichi.A., Takeda.S., Watanabe.T., Takahashi.E., Hirai.Y., Maekawa.H., Shin.S. and Nakamura.Y.
TITLE Unpublished(303)
JOURNAL Unpublished (1995)
REFERENCE 2 (bases 1 to 293)
AUTHORS Fujiwara.T.
TITLE Direct Submission
JOURNAL Submitted (30-MAY-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,

Japan (Tel:0886-65-2888, Fax:0886-37-1035)

Submitted (30-May-1995) to DDBJ by:

Tsutomu Fujiwara

Otsuka GEN Research Institute

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Tokushima, Tokushima

771-01

Japan

Phone: 0886-65-2888

Fax : 0886-37-1035.

Location/Qualifiers

1..293

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Clontech human aorta polyA+ mRNA (#6572)"

102 a 51 c 26 g 109 t 5 others

BASE COUNT

ORIGIN

Query Match 14.3%; Score 290; DB 6; Length 293;

Best Local Similarity 98.0%; Pred. No. 0.00e+00;

Matches 287; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 1 TCACATTCAGCTACATCTCCATTTATTAGAGGACATTAACCATTTCTATAGCATG 50
|||||Qy 1710 TCACATTCAGCTACATCTCCATTTATTAGAGGACATTAACCATTTCTATAGCATG 1769
|||||Db 61 ATTCTTCAAGTAAAGGCAAAAGATATAATFYYYATTAATTCACCTTGAGTACTTTAAGGC 120
|||||Qy 1770 ATTCTTCAAGTAAAGGCAAAAGATATAATFYYYATTAATTCACCTTGAGTACTTTAAGGC 1829
|||||Db 121 TGTTTAAACATTTCTTACTTAACCTTTTGCAAAATTAACCCATTTAGCTTACCTGTA 180
|||||Qy 1830 TGTTTAAACATTTCTTACTTAACCTTTTGCAAAATTAACCCATTTAGCTTACCTGTA 1889
|||||Db 181 TATACATAGTAGTTTACCTTTAAAGAGTTGTAATAATATGCTTTAACCAACACTGTAAT 240
|||||Qy 1890 TATACATAGTAGTTTACCTTTAAAGAGTTGTAATAATATGCTTTAACCAACACTGTAAT 1949
|||||Db 241 ATTTCAGATAAACATTTATATCTTGTATATTAACCTTTACATCTGTTTACCT 293
|||||Qy 1950 ATTTCAGATAAACATTTATATCTTGTATATTAACCTTTACATCTGTTTACCT 2002
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RESULT 47 HUM238C05B 293 bp mRNA EST 21-MAY-1996

LOCUS Human aorta cDNA 5'-end GEN-238C05, mRNA sequence.

DEFINITION

ACCESSION D62098

NID 9965874

KEYWORDS EST; EST(expressed sequence tag); Human aorta; similar to none(May 29, 1995).

SOURCE Homo sapiens cDNA to mRNA, clone_lib:Clontech human aorta polyA+ mRNA (#6572).

ORGANISM Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;

Homo.

REFERENCE 1 (bases 1 to 293)

AUTHORS Fujiwara.T., Hirano.H., Katagiri.T., Kawai.A., Kuga.Y., Nagata.M., Okuno.S., Ozaki.K., Shimizu.F., Shimada.Y., Shinomiya.H., Takaichi.A., Takeda.S., Watanabe.T., Takahashi.E., Hirai.Y., Maekawa.H., Shin.S. and Nakamura.Y.

TITLE Unpublished(303)

JOURNAL Unpublished (1995)

REFERENCE 2 (bases 1 to 293)

AUTHORS Fujiwara.T.

TITLE Direct Submission

JOURNAL Submitted (30-MAY-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,

Japan (Tel:0886-65-2888, Fax:0886-37-1035)
Submitted (30-May-1995) to DDBJ by:

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Otsuka Pharmaceutical Co.,Ltd
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Tokushima, Tokushima
771-01

Japan
Phone: 0886-65-2888
Fax : 0886-37-1035.

FEATURES source
1. 299 Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 104 a 51 c 28 g 112 t 4 others
ORIGIN /clone_lib="Clontech human aorta polyA+ mRNA (#6572)"

Query Match 14.2%; Score 287; DB 6; Length 299;
Best Local Similarity 98.0%; Pred. No. 0.00e+00;

Matches 295; Conservative 4; Mismatches 0; Indels 2; Gaps 2;

Db 1 TACATGATACATCCAGCTACATCTCCATTTCCATTTATTAGAGCACATTAACCATTTCT 60
|||||
Qy 1702 TACATGATACATCCAGCTACATCTCCATTTATTAGAGCACATTAACCATTTCT 1761
|||||
Db 61 ATAGCATGATTTCTCAAGTAAAGGCAAAAGATATAATTTTATAATTGACTTGAGTAC 120
|||||
Qy 1762 ATAGCATGATTTCTCAAGTAAAGGCAAAAGATATAATTTTATAATTGACTTGAGTAC 1821
|||||
Db 121 TTTAAGCCTGTTTAAACATTTCTTAACTTTGCAAAATTAACCCATTTAGCTT 180
|||||
Qy 1822 TTTAAGCCTGTTTAAACATTTCTTAACTTTGCAAAATTAACCCATTTAGCTT 1881
|||||
Db 181 ACCYGTATATACATAGTAGTTTACCTTTAAAGTTGTAARA-TATTGCTTTAAACCA 239
|||||
Qy 1882 ACCYGTATATACATAGTAGTTTACCTTTAAAGTTGTAARAATATGCTTTAAACCA 1941
|||||
Db 240 CTGTAATATTTTCAGATAAACATTTATTTCTGTATATAAACT-ACATCCCTGTTTACC 298
|||||
Qy 1942 CTGTAATATTTTCAGATAAACATTTATTTCTGTATATAAACTTTACATCCCTGTTTACC 2001
|||||
Db 299 T 299
Qy 2002 T 2002

RESULT 50 HUM289F09B 287 bp mRNA EST 21-MAY-1996
LOCUS Human aorta cDNA 5'-end GEN-289F09, mRNA sequence.
DEFINITION D62477
ACCESSION 966253
NID
KEYWORDS EST; EST(expressed sequence tag); Human aorta; similar to none(May 29,1995).
SOURCE Homo sapiens cDNA to mRNA, clone_lib:Clontech human aorta polyA+ mRNA (#6572).
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 287)
AUTHORS Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y., Maekawa,H., Shin,S. and Nakamura,Y.
JOURNAL Unpublished(303)
REFERENCE 2 (bases 1 to 287)
AUTHORS Fujiwara,T.
TITLE Direct Submission
JOURNAL Submitted (30-MAY-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical

Co.,Ltd: 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
Japan (Tel:0886-65-2888, Fax:0886-37-1035)
Submitted (30-May-1995) to DDBJ by:

Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 Kagasuno Kawauchi-cho
Tokushima, Tokushima
771-01

Japan
Phone: 0886-65-2888
Fax : 0886-37-1035.

FEATURES source
1. 287 Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 99 a 50 c 33 g 105 t
ORIGIN /clone_lib="Clontech human aorta polyA+ mRNA (#6572)"

Query Match 14.1%; Score 285; DB 6; Length 287;
Best Local Similarity 99.7%; Pred. No. 0.00e+00;

Matches 286; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 TCAGACTCAGTCTTAAGTCTTACACAAATTCATCATTTTATACCTTCAATGGGAACCTTA 60
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Qy 1636 TCAGACTCAGTCTTAAGTCTTACACAAATTCATCATTTTATACCTTCAATGGGAACCTTA 1695
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Db 61 AACTGTTACATCTATCACATTCAGCTACAACTTCCATTTATTAGAGCACATTAAC 120
|||||
Qy 1696 AACTGTTACATCTATCACATTCAGCTACAACTTCCATTTATTAGAGCACATTAAC 1755
|||||
Db 121 ATTCTATAGCATGATTTCTTCAAGTAAAGGCAAAAGATATAAAATTTTATATTGACIT 180
|||||
Qy 1756 ATTCTATAGCATGATTTCTTCAAGTAAAGGCAAAAGATATAAAATTTTATATTGACIT 1815
|||||
Db 181 GAGTACTTTAAGCCTTGTTTAAACATTTCTTACTTAACATTTTGGCAAATTAACCCATTG 240
|||||
Qy 1816 GAGTACTTTAAGCCTTGTTTAAACATTTCTTACTTAACATTTTGGCAAATTAACCCATTG 1875
|||||
Db 241 TAGCTTACCTGTAATATACATAGTAGTTTACCTTTAAAGGTTGTAA 287
|||||
Qy 1876 TAGCTTACCTGTAATATACATAGTAGTTTACCTTTAAAGGTTGTAA 1922
|||||

RESULT 51 HUM343G04B 281 bp mRNA EST 15-DEC-1995
LOCUS Human aorta cDNA 5'-end GEN-343G04, mRNA sequence.
DEFINITION D79867
ACCESSION g1180218
NID
KEYWORDS EST; EST(expressed sequence tag); Human aorta.
SOURCE Homo sapiens aorta cDNA to mRNA, clone_lib:human aorta polyA+.
ORGANISM Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 281)
AUTHORS Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y., Maekawa,H., Shin,S. and Nakamura,Y.
JOURNAL Large-scale sequencing project at Otsuka GEN Research Institute
REFERENCE 2 (bases 1 to 281)
AUTHORS Fujiwara,T.
TITLE Direct Submission

JOURNAL Submitted (07-NOV-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical Co.,Ltd, 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01, Japan
COMMENT Submitted (7-Nov-1995) to DDBJ by: Tsutomu Fujiwara Otsuka GEN Research Institute

Otsuka Pharmaceutical Co.,Ltd
463-10 Kagasuno Kawauchi-cho
Tokushima, Tokushima
771-01
Japan
Phone: 0886-65-2888
Fax : 0886-37-1035.

FEATURES
source
Location/Qualifiers
1. .281

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="human aorta polyA"
/tissue_type="aorta"

BASE COUNT 101 a 45 c 24 g 110 t 1 others
ORIGIN

Query Match 13.8%; Score 279; DB 6; Length 281;

Best Local Similarity 99.3%; Pred. No. 0.00e+00;

Matches 279; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 TACAATATCTTCATTATAGAGCACATTAACCAATTTCTATAGCATGATTTCTTCAAGT 60

Qy 1722 TACAATCTTCATTATAGAGCACATTAACCAATTTCTATAGCATGATTTCTTCAAGT 1781

Db 61 AAAGGCAAAAGATATAAATTTTATAATTGACTTGAGTACTTTAAGCCTTGTTAAACA 120

Qy 1782 AAAGGCAAAAGATATAAATTTTATAATTGACTTGAGTACTTTAAGCCTTGTTAAACA 1841

Db 121 TTCTTACTTAACTTTGCAATTAACCCATTGTAGCTTACCTGTAATATACATAGTAG 180

Qy 1842 TTCTTACTTAACTTTGCAATTAACCCATTGTAGCTTACCTGTAATATACATAGTAG 1901

Db 181 TTACCTTTAAAGTGTAAAAATATTGCTTTAAACAACACGTGAATATTTTCAGATAAA 240

Qy 1902 TTACCTTTAAAGTGTAAAAATATTGCTTTAAACAACACGTGAATATTTTCAGATAAA 1961

Db 241 CATTATATCTTKATATAAATTTACATCCCTTTTACCT 281

Qy 1962 CATTATATCTTKATATAAATTTACATCCCTTTTACCT 2002

RESULT 52

LOCUS HUM233G01B 273 bp mRNA EST 21-MAY-1996

DEFINITION Human aorta cDNA 5'-end GEN-233G01, mRNA sequence.

ACCESSION D62031

NID 995807

KEYWORDS EST: EST(expressed sequence tag); Human aorta; similar to none(May 29,1995).

SOURCE Homo sapiens cDNA to mRNA, clone_lib:Clontech human aorta polyA+ mRNA (#6572).

ORGANISM Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;

Homo.

REFERENCE 1 (bases 1 to 273)

AUTHORS Fujiwara,T., Hirano,H., Katagiri,T., Kawai,A., Kuga,Y., Nagata,M.,

Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H.,

Takaichi,A., Takeda,S., Watanabe,T., Takahashi,E., Hirai,Y.,

Maekawa,H., Shin,S. and Nakamura,F.

Unpublished(303)

REFERENCE 2 (bases 1 to 273)

AUTHORS Fujiwara,T.

Unpublished(303)

REFERENCE 3 (bases 1 to 273)

AUTHORS Fujiwara,T.

Unpublished(303)

REFERENCE 4 (bases 1 to 273)

AUTHORS Fujiwara,T.

Unpublished(303)

REFERENCE 5 (bases 1 to 273)

AUTHORS Fujiwara,T.

Unpublished(303)

REFERENCE 6 (bases 1 to 273)

AUTHORS Fujiwara,T.

Unpublished(303)

Tokushima, Tokushima
771-01
Japan
Phone: 0886-65-2888
Fax : 0886-37-1035.

FEATURES
source
Location/Qualifiers
1. .273

/organism="Homo sapiens"
/db_xref="taxon:9606"

/clone_lib="Clontech human aorta polyA+ mRNA (#6572)"
BASE COUNT 100 a 43 c 25 g 99 t 6 others
ORIGIN

Query Match 13.5%; Score 273; DB 6; Length 273;

Best Local Similarity 97.8%; Pred. No. 0.00e+00;

Matches 267; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Db 1 ATCACATTCAGCTACAATACCTTCATTTATTAGAACGACATTAAACCATTTCTATAGCAT 60

Qy 1709 ATCACATTCAGCTACAATACCTTCATTTATTAGAACGACATTAAACCATTTCTATAGCAT 1768

Db 61 GATTTCTTCAAGTAAAGGCAAAAGATATAAATYYBATAATTVMTTGAGTACTTTAAGC 120

Qy 1769 GATTTCTTCAAGTAAAGGCAAAAGATATAAATTTTATAATTCAGTCTGAGTACTTTAAGC 1828

Db 121 CTGTGTTAAACATTTCTTACTTAACTTTTGCAAAATTAACCCATTTGAGTCTTACCTGTGA 180

Qy 1829 CTGTGTTAAACATTTCTTACTTAACTTTTGCAAAATTAACCCATTTGAGTCTTACCTGTGA 1888

Db 181 ATATACATAGTAGTTTACCTTTAAAGTTGTAAAAATATTGCTTTTAAACCAACACTGTAAA 240

Qy 1889 ATATACATAGTAGTTTACCTTTAAAGTTGTAAAAATATTGCTTTTAAACCAACACTGTAAA 1948

Db 241 TATTTTCAGATAAACATTATATCTTCTGTATATAA 273

Qy 1949 TATTTTCAGATAAACATTATATCTTCTGTATATAA 1981

RESULT 53

LOCUS AA3711169 276 bp mRNA EST 21-APR-1997

DEFINITION EST83193 Prostate gland I Homo sapiens cDNA 5' end, mRNA sequence.

ACCESSION AA3711169

NID 92023731

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;

Homo.

REFERENCE 1 (bases 1 to 276)

AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,

Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,

White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,

Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,

Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,

Glocke,A., Gnchm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,

Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,

Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,

Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,

Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,

Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,

Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,

He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,

Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,

Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,

Dillion,L.M., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,

Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

Other ESTs: THC180057

CONTACT: Kerlavage, AR

TITLE

JOURNAL

MEDLINE

COMMENT

Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES

source
1. .276
/organism="Homo sapiens"
/note="Organ: prostate; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
/db_xref="ATCC (inhost):175811"
/db_xref="taxon:9606"
/clone_lib="Prostate gland I"
/sex="male"
/dev_stage="adult, 21 yrs"
<1. .276
52 a 92 c 72 g 60 t

BASE COUNT

ORIGIN
Query Match 13.5%; Score 274; DB 5; Length 276;
Best Local Similarity 99.6%; Pred. No. 0.00e+00;
Matches 275; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 1 GTGATCACTCGGTGAAGCGGTGCAGAGGGGCGAGAGAGTTCAAGCGCATCTCCCGC 60
QY 1060 GTGATCACTCGGTGAAGCGGTGCAGAGGGGCGAGAGAGTTCAAGCGCATCTCCCGC 1119
Db 61 AGCATCCGCAAGCTGCAGTGTCTAGTCCCGGCATCTTATGCTCCGACAGGCGTGTCTCA 120
QY 1120 AGCATCCGCAAGCTGCAGTGTCTAGTCCCGGCATCTTATGCTCCGACAGGCGTGTCTCA 1179
Db 121 GAGCAGCGCTGACCATTTCTGCTCCGGATCTCAGTCCCGTTCCTCCCAAGCACACTCTTA 180
QY 1180 GAGCAGCGCTGACCATTTCTGCTCCGGATCTCAGTCCCGTTCCTCCCAAGCACACTCTTA 1239
Db 181 GTGCTCCAGTCTCAGCTGGGAGCTTCCCGTTCCTCCCGTTCCTCCCGTTCCTCCCGTTC 240
QY 1240 GTGCTCCAGTCTCAGCTGGGAGCTTCCCGTTCCTCCCGTTCCTCCCGTTCCTCCCGTTC 1299
Db 241 ATTCTCTAGTTATTAAGCCACAGGAGTGGATAGCT 276
QY 1300 ATTCTCTAGTTATTAAGCCACAGGAGTGGATAGCT 1335

RESULT 54
LOCUS AA339113 282 bp mRNA EST 21-APR-1997
DEFINITION EST44185 Fetal brain I Homo sapiens cDNA 5' end, mRNA sequence.
ACCESSION AA339113
NID g191371
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
Homo.
1 (bases 1 to 282)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fritchman,J.L., Geonhagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palmanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,

He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280
Other_ESTs: THC180057
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES

source
1. .282
/organism="Homo sapiens"
/note="Organ: brain; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
/db_xref="ATCC (inhost):140742"
/db_xref="taxon:9606"
/clone_lib="Fetal brain I"
/sex="female"
/dev_stage="fetus, 24 wks"
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69 a 70 c 56 g 82 t 5 others

BASE COUNT

ORIGIN
Query Match 13.5%; Score 273; DB 4; Length 282;
Best Local Similarity 97.5%; Pred. No. 0.00e+00;
Matches 275; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Db 1 TTCTGCTCCGGATCTCAGCTCCCGTTCCTCCCAAGCACAGTCTCAGTCTCAGTCTCAG 60
QY 1196 TTCTGCTCCGGATCTCAGCTCCCGTTCCTCCCAAGCACAGTCTCAGTCTCAGTCTCAG 1255
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QY 1256 CCTGGGAGCTTCCCGTTCCTGTCAGTTCATCCCGACAGTTCCTGAGTTATAA 1315
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QY 1316 GCCACAGGAGTNGTAGTGTGTTTTCACCTAAAGAAAGCCACCGAATCTTGTA 1375
Db 181 ATATTCAACTAATAAATCATGAATATTTTATGAAGTTAAAGTACGTCACCTTTAA 240
QY 1376 ATATTCAACTAATAAATCATGAATATTTTATGAAGTTAAAGTACGTCACCTTTAA 1435
Db 241 GCTAGTTTGTANTAGTGCAACTNTGACTTGGGTCTGGTGG 282
QY 1436 GCTAGTTTGTANTAGTGCAACTNTGACTTGGGTCTGGTGG 1477

RESULT 55
LOCUS C16543 283 bp mRNA EST 04-SEP-1996
DEFINITION Human aorta cDNA 5'-end GEN-347D02, mRNA sequence.
ACCESSION C16543
NID g1571250
KEYWORDS EST; EST(expressed sequence tag); Human aorta.
SOURCE Homo sapiens aorta cDNA to mRNA, clone:347D02.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
Homo.
1 (sites)
Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y.,

Kyushiki, H., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y.,
Shinomiya, H., Suzuki, M., Takaichi, A., Takeda, S., Watanabe, T.,
Maekawa, H., Nakamura, Y. and Takahashi, E.

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Otsuka CDNA Project
Unpublished (1996)
2 (bases 1 to 283)
Direct Submission

Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases, Tsutomu
Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical
Co., Ltd, 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
Japan (Tel: +81-886-65-2888, Fax: +81-886-37-1035)
Location/Qualifiers

FEATURES
source

1. .283
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="347D02"
/tissue-type="aorta"

BASE COUNT 101 a 46 c 26 g 110 t

ORIGIN

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Best Local Similarity 99.3%; Pred. No. 0.00e+00;
Matches 281; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Db 1 TACAATACATCCATTTATTAGAGCACATTAAACCATTTCTATAGCATGATTTCTTCAAGT 60

QY 1722 TACAATACATCCATTTATTAGAGCACATTAAACCATTTCTATAGCATGATTTCTTCAAGT 1781

Db 61 AAAAGCAAAAGATATAAATTTATATATGACCTGAGTACTTTAAAGCCTGTTTAAACA 120

QY 1782 AAAAGCAAAAGATATAAATTTATATATGACCTGAGTACTTTAAAGCCTGTTTAAACA 1841

Db 121 TTCTTACTTACTTTTGGCAATTAACCCATTTGACCTGACCTGTAATATACATAGTAG 180

QY 1842 TTCTTACTTACTTTTGGCAATTAACCCATTTGACCTGACCTGTAATATACATAGTAG 1901

Db 181 TTACCTTTAAAGTTGTAATAATATGCTTTAACCAACACCTGTAATATTTTCAGATA 240

QY 1902 TTACCTTTAAAGTTGTAATAATATGCTTTAACCAAC-ACGTGTAATATTTTCAGATA 1960

Db 241 ACATTATATCTTGATATAAATTTTACATCCTGTTTACCT 283

QY 1961 ACATTATATCTTGATATAAATTTTACATCCTGTTTACCT 2002

RESULT 56

LOCUS AA176165 262 bp mRNA EST 30-DEC-1996
DEFINITION zp23hl2.s1 Stragene neuroepithelium (#937231) Homo sapiens CDNA
clone 610343 3', mRNA sequence.

ACCESSION AA176165

NID g1757287

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata;

Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 262)

AUTHORS Hillier, L., Clark, N., Dubucque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E.,

Waterson, R., Williamson, A., Wohldmann, P. and Wilson, R.

WashU-Merck EST Project

Unpublished (1995)

TITLE

JOURNAL

COMMENT

Contact: Wilson RK

WashU-Merck EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13.fwd. from Amersham
High quality sequence stop: 161.

FEATURES
source

1. .262
Location/Qualifiers

/organism="Homo sapiens"

/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:

XhoI; Cloned unidirectionally. Primer: Oligo dt. NT2

cells (Ntera-2/cl.D1) induced with Retinoic Acid for 24

hours. Average insert size: 1.5 kb; Uni-ZAP XR vector; -5'

adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor

sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT 3'

/db_xref="taxon:9606"

/clone="610343"

/clone_lib="Stratagene neuroepithelium (#937231)"

/dev_stage="Ntera-2/RA neuroepithelial cells"

/lab_host="SOLR (kanamycin resistant)"

complement(<1. >262)

BASE COUNT 100 a 27 c 40 g 91 t 4 others

ORIGIN

Query Match 12.6%; Score 256; DB 25; Length 262;

Best Local Similarity 98.1%; Pred. No. 0.00e+00;

Matches 257; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 1 GGTAACACAGATGTAAGTTTATATACAGAATATATGTTATCTCGAAATATTTACAG 60

Cp 2001 GGTAACACAGATGTAAGTTTATATACAGAATATATGTTATCTCGAAATATTTACAG 1942

Db 61 TGTGGTTAAAGCAATATTTTACAACCTTTTAAAGGTAAACTACTATGTATTACAGGT 120

Cp 1941 TGTGGTTAAAGCAATATTTTACAACCTTTTAAAGGTAAACTACTATGTATTACAGGT 1882

Db 121 AAGCTACAATGGGTTTAAATTTGCAAAAGTTAAGTAAGAAATGTTTTTAAACAAGCTTAAA 180

Cp 1881 AAGCTACAATGGGTTTAAATTTGCAAAAGTTAAGTAAGAAATGTTTTTAAACAAGCTTAAA 1822

Db 181 GTACTCAAGTCAATATAAATTTATANCCTTTNGCCCTTTTACTTGAGAAATCATGCTAT 240

Cp 1821 GTACTCAAGTCAATATAAATTTATANCCTTTNGCCCTTTTACTTGAGAAATCATGCTAT 1762

Db 241 AGAAATGGNTAATGTCCTCTA 262

Cp 1761 AGAAATGGNTAATGTCCTCTA 1740

RESULT 57

LOCUS HUM286A04B 263 bp mRNA EST 14-DEC-1995
DEFINITION Human aorta cDNA 5'-end GEN-286A04, mRNA sequence.

ACCESSION D79597

NID g1179948

KEYWORDS EST; EST(expressed sequence tag); Human aorta.

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata;

Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;

Homo.

REFERENCE 1 (bases 1 to 263)

AUTHORS Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Negata, M.,

Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H.,

Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y.,

Maekawa, H., Shin, S. and Nakamura, Y.

Large-scale sequencing project at Otsuka GEN Research Institute

Unpublished (1995)

REFERENCE 2 (bases 1 to 263)

AUTHORS Fujiwara, T.

Direct Submission

TITLE

JOURNAL

COMMENT

Submitted (07-NOV-1995) to the DDBJ/EMBL/GenBank databases. Tsutomu

Fujiwara, Otsuka GEN Research Institute, Otsuka Pharmaceutical

Co., Ltd, 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,

Japan

Submitted (7-Nov-1995) to DDBJ by:

Tsutomu Fujiwara

Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project


```

1 STATE: MA
2 COUNTRY: USA
3 ZIP: 02140
4
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: Floppy disk
7 COMPUTER: IBM PC compatible
8 OPERATING SYSTEM: PC-DOS/MS-DOS
9 SOFTWARE: Patent In Release #1.0, Version #1.25
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/08/848,439
12 FILING DATE:
13 CLASSIFICATION: 435
14 ATTORNEY/AGENT INFORMATION:
15 NAME: LAZAR, STEVEN R.
16 REGISTRATION NUMBER: 32,618
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: (617) 498-8260
19 TELEFAX: (617) 876-5851
20 INFORMATION FOR SEQ ID NO: 3:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 275 amino acids
23 TYPE: amino acid
24 STRANDEDNESS: single
25 TOPOLOGY: linear
26
27 MOLECULE TYPE: protein
28 Reverse translation from the peptide US-08-848-439-3.
29 ; Note: the original peptide US-08-848-439-3 contained at least one of
30 ; the residues Arg, Ile, Leu, or Ser. The nucleic acid sequence
31 ; thus contains ambiguous bases which may translate into amino acids
32 ; other than the original amino acids.
33
34 848439-3-trans
35 WSNCGNCGNGNTTYNTTYNTTGGNCARCCNGAYTTYSNTAYAAARMGNWSNAAYTGYAARCCNATNCC
36 CNGNAAYYTNCARYTNTGYACGNGATNAGTAYCARAAATACMGNTYNTCCNAAYYTNTGNCNCAYGA
37 RACNATGAARGACTYNTGYCARCCNGCGNCGTGGATCCNCTNGTNTATCAARGCARTGYCAYCCNGAY
38 ACGAARAARATYYTNTGWSNTYNTTGGCNCNGTYYTNGAYGYTNGAYGARACNATNCCARCNT
39 GYCAWSYNTTGYTGCNCACTNAGARGMNTGYCCNCGTATGWSNGCNTTYGGNTTYCCTGGCC
40 NGAYATGYTNGARTGYGAYMGNTTTCNCARGAAYAYGYTNTGATGCCNTYNTGWNWSNMGAYCAY
41 YTYNTCCNCGNANGARGCNGCCNARGTNTGYGARGCNTGYAARAAYAAAYGAYGAYGAYG
42 AYATNATGACACNTNTYNTAABRAGYATTYTGCNTYNAARATNAAAGTNAARGATNACNTAYATNAA
43 YMGNGAYACNAAATNATNTYGAARGAARWNAARACNATNTAARAYTNAAYCGGNTMWSNARGMN
44 GAYTYAARARHSNGTYNTTGGTYNAAACAYWSYNTTCARTCYACNTGYCARGARATCAAYGAYATNA
45 ATYGCNCTAYTNTGNTATGGNCARCAARCGGNGGNGTNGTNTATNACNWSNGTNAARMGNTGGCA
46 RAARGNCARGMNGNTTYAARMGNATNWSNNGWGNATNMGNAARYTNCARTGY1

```

WAP5REH

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPSrch_nm n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 9 09:05:57 1997; MasPar time 98.26 Seconds

Tabular output: not generated. 940.036 Million cell updates/sec

Title: >848439-2-trans

Description: (1-885) from translate.seq

Perfect Score: 734

N.A. Sequence: 1 ATGTCNARGCGCGCGNWS.....SNATNGNAARYTNCARTGY 885
Comp: TACRANGTYCCGCGCGNWS.....WNTANKNTTYRANGTYACR

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 142080 seqs, 52183452 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: n-geneseq28

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 11.471; Variance 13.768; scale 0.833

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query	ID	Description	Pred. No.
1	128	17.4	1047	2	Human Natriuretic Pep	2.49e-29
2	107	14.6	1047	2	Human Natriuretic Pep	2.17e-22
3	53	7.2	501	3	Sequence encoding new	2.05e-05
4	53	7.2	501	3	Sequence encoding new	2.05e-05
5	53	7.2	565	6	HCV envelope region n	2.05e-05
6	52	7.1	501	3	Sequence encoding new	4.03e-05

c	7	51	6.9	498	3	N50034	Sequence encoding new	7.88e-05
c	8	51	6.9	501	3	N50023	Sequence encoding new	7.88e-05
c	9	51	6.9	501	3	N50028	Sequence encoding new	7.88e-05
c	10	50	6.8	501	3	N50031	Sequence encoding new	1.54e-04
c	11	50	6.8	501	3	N50023	Sequence encoding new	1.54e-04
c	12	50	6.8	501	3	N50029	Sequence encoding new	1.54e-04
c	13	49	6.7	501	3	N50024	Sequence encoding new	2.99e-04
c	14	49	6.7	501	3	N50032	Sequence encoding new	2.99e-04
c	15	49	6.7	501	3	N50025	Sequence encoding new	2.99e-04
c	16	49	6.7	501	3	N50024	Sequence encoding new	2.99e-04
c	17	49	6.7	984	17	Q94336	Degenerate Alteromona	2.99e-04
c	18	48	6.5	501	3	N50026	Sequence encoding new	5.80e-04
c	19	47	6.4	498	3	N50034	Sequence encoding new	1.12e-03
c	20	47	6.4	501	3	N50031	Sequence encoding new	1.12e-03
c	21	47	6.4	501	3	N50029	Sequence encoding new	1.12e-03
c	22	17	6.4	501	3	N50032	Sequence encoding new	1.12e-03
c	23	47	6.4	501	3	N50032	Sequence encoding new	1.12e-03
c	24	45	6.1	501	3	N50027	Sequence encoding new	4.13e-03
c	25	45	6.1	501	3	N50030	Sequence encoding new	4.13e-03
c	26	45	6.1	501	3	N50033	Sequence encoding new	4.13e-03
c	27	45	6.1	565	6	Q35072	HCV envelope region n	4.13e-03
c	28	43	5.9	501	3	N50026	Sequence encoding new	1.50e-02
c	29	42	5.7	204	1	N81164	Base substituted E.co	2.84e-02
c	30	41	5.6	204	1	N81164	Base substituted E.co	5.36e-02
c	31	41	5.6	657	7	Q43519	Degenerate FMN reduct	5.36e-02
c	32	41	5.6	657	7	Q43519	Degenerate FMN reduct	5.36e-02
c	33	41	5.6	711	15	Q88282	V.fischeri flavin red	5.36e-02
c	34	41	5.6	984	17	Q94336	Degenerate Alteromona	5.36e-02
c	35	40	5.4	91	9	Q51746	Oligonucleotide probe	1.01e-01
c	36	40	5.4	3871	2	N71302	HSV-1 gB and surround	1.01e-01
c	37	39	5.3	91	9	Q51746	Oligonucleotide probe	1.88e-01
c	38	39	5.3	501	3	N50025	Sequence encoding new	1.88e-01
c	39	39	5.3	774	3	Q22981	Gelonin toxin DNA	1.88e-01
c	40	39	5.3	1065	17	Q94335	Degenerate Alteromona	1.88e-01
c	41	39	5.3	3871	2	N71302	HSV-1 gB and surround	1.88e-01
c	42	37	5.0	711	15	Q88282	V.fischeri flavin red	6.45e-01
c	43	37	5.0	1065	17	Q94335	Degenerate Alteromona	6.45e-01
c	44	35	4.8	420	14	Q88233	Bovine aFGF synthetic	2.17e+00
c	45	34	4.6	420	14	Q88233	Bovine aFGF synthetic	3.93e+00

ALIGNMENTS

RESULT	1
ID	Q10572 standard; DNA; 1047 BP.
AC	Q10572;
DT	09-APR-1991 (first entry)
DE	Human Natriuretic Peptide Receptor B.
KW	NPBR; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;
KW	hyperaldosteronism; glaucoma; guanyl cyclase.
OS	Homo sapiens.
PH	Key Location/Qualifiers
FT	Peptide 1..22
FT	/label= signal sequence
FT	Protein 12
FT	/label= mature NPBR
FT	Domain 23..455
FT	/label= extracellular domain
FT	/note= "binds natriuretic peptides A, B and C"
FT	Domain 456..456
FT	/label= transmembrane domain
FT	Domain 479..1047
FT	/label= cytoplasmic domain
FT	/note= "GC and protien kinase activity"

FT	Modified-site 24..26	
FT	/label= N-glycosite	
FT	Modified-site 35..37	
FT	/label= N-glycosite	
FT	Modified-site 161..163	
FT	/label= N-glycosite	
FT	Modified-site 195..197	
FT	/label= N-glycosite	
FT	Modified-site 244..246	
FT	/label= N-glycosite	
FT	Modified-site 277..279	
FT	/label= N-glycosite	
FT	Modified-site 349..351	
FT	/label= N-glycosite	
FT	Modified-site 600..602	
FT	/label= N-glycosite	
PN	MO3100202-A	
PD	10-JAN-1991.	
PF	22-JUN-1990; U03586.	
PR	23-JUN-1989; US-370673.	
PA	(GETH) GENENTECH INC.	
PI	Chang M, Goeddel D, Lowe D;	
PI	WPI; 91-036711/05.	
DR	N-PSDB; Q10324.	
CC	The sequence was derived from the DNA encoding natriuretic peptide	
CC	receptor B, NPRB, having guanyl cyclase (GC) activity and protein	
CC	kinase activity. The DNA can be inserted into expression vectors	
CC	for the prodn. of the protein, opt. after being mutated to produce	
CC	NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr=	
CC	114, 952). The protein (or variants) can be used in treatment of	
CC	natriuretic peptide disorders, and also to isolate peptides using	
CC	affinity chromatography. Antibodies with affinity for NPRB can	
CC	also be prepd.	
SC	Sequence 1047 BP; 87 A; 15 C; 83 G; 51 T;	
	Query Match 17.4%; Score 128; DB 2; Length 1047;	
	Best Local Similarity 12.3%; Pred. No. 2,49e-29;	
	Matches 108; Conservative 244; Mismatches 518; Indels 8; Gaps 8;	
Db	114 hwrnmntagavagsgakndhyrtvrtgnaekngnvvvthghnnwtaraannyda 173	
Qy	: : : : : : : : : : : : : : : :	
	7 CARGCGCCGCGNSNYTNTYNTYNTTYTTCGNCNSCAVYTGTYTTCGNGWSGCGN 66	
Db	174 rtdtrrhntngvnmangnsnvhvyarngngnnnathmrangrinvnycgngnnm 233	
Qy	: : : : : : : : : : : : : : : : : :	
	67 MCGNGNYNTTYTNTTYTCGNCARCGCAYTYSWTAYAAARMGWSNAAVTCYAAACGN 126	
Db	234 hnnnnnannrntngdyvnyyndvngsnragnrtatrgnwdnrtnnanannrnnntv 293	
Qy	: : : : : : : : : : : : : : : : : : : : : :	
	127 ATWCNGCNGAAAYTN-CARYTNTGYCAYGNGATNGARTACARAAVATGCGNTYTCNAA 185	
Db	294 nvntyrnnnnnnnnnnrnnrnnrdngvnnngnennnnnagcnydgnyyannvnnntnn 353	
Qy	: : : : : : : : : : : : : : : : : : : : :	
	186 YTYTNTTCGNCAYGAACNATGAARGA-RGTNYTNGCARCGCGNGCGNTGGATTCN 244	
Db	354 nggtrndgrrnrvknmrgryghvrtgmvmdkndrntcdvnmwngdndsgdnnaahysg 413	
Qy	: : : : : : : : : : : : : : : : : : : :	
	245 TNGTNATGAARCAARTGYCAYCGGAYACAAARAARTTYTNTTCYWSNYTNTTYTCNC 304	
Db	414 anknnwrtgrnnrvkvgnndnncandnddscdktnstnnanvngtgnctnnmngvs 473	
	: : : : : : : : : : : : : : : : : : : : : :	

Qy	335	T T T Y T T G A G A Y Y T T G A G A R A C A T N T C A R C C T G C A Y S Y N T T G T G T N C A R G T N A	364
Db	474	snnnrkmmnnknnaemw-rnrwnnnngnsnyhkgagernstnsrsgesgenmtahg	532
Qy	365	ARGAYMGNTTGGCCNCNGTATGMSGNCNTTYGGNTTYTCNTGCCNGAYATGYTNGART	424
Db	533	kynnnaantghknvgnvaankvhnkrrnntnrvmnnknkhrdvmnnhntrrngaecdnnnn	592
Qy	425	G Y G A Y M G N - T T Y C N C A R G A A A Y G A Y T T N T G Y A T N C C N Y T M G C N W S N S G A Y C A Y Y T T	483
Db	593	cyvtvncrgsmndnnndnnrnyrsnnndvknvkmannhnsnashghskesncvv	652
Qy	484	Y T N C N G C N A C N G A R G C C C N A A R G T N T G Y G - A R G C N T C Y A A R A A Y A A R A A Y G A Y G A	542
Db	653	dsvrvnknktdygnasretanddnnyakknntamnnsgnnnttgmnaadvyengn	712
Qy	543	Y G A Y A A Y G - A Y A T N A T G G A R A C N Y T N T G Y A A R A A Y G A Y T T Y C C N Y T N A A R A T N A A R G T N A	601
Db	713	nnnnnnszgnnyungndnsknvknvkrngnrnyrnrsndrtnnnnnnvnmrncwand	772
Qy	602	ARGARATWACNTATYATNAYTMGNGAYACNAARAATNATNTYNGARACNAARWNSAARACNA	661
Db	773	nanrndngnnknrrnkngtlenndnnnnrnmvannnnknvnrntnaynnnkrkana	832
Qy	662	TNTAYAARYTNAAYGGCTNWSHGARMGNGAYTTNAARAARHSNGTNYTNGGYTN-AAR	720
Db	833	nyvnnnhsvannkrgntvnanandvrvnsydsdvngtansanstmmvvtvnnndytc	892
Qy	721	G A Y S N Y T N C A R T G Y A C N T G Y G A R G A R A T G A A Y G A Y A T N A A Y G C N C A Y T T Y T N G T N A T G	780
Db	893	ndamdnndykvntngdaymwvsgnngngrngnthainmarmanndavesnrnrhrhd	952
Qy	781	GCNCARARCARCGN--GGNGARYTNGTATWACNWSNGTNAARWNTGCCAARAGGNCA	839
Db	953	nnrnngvhtgnvcagvgvgnkmmirycnngdvtvtaerm	990
Qy	840	RMNGARTTYAARMGNATNWSNMGNSATNMGNAARY	877
RESULT 2			
ID	Q10572	standard; DNA; 1047 BP.	
AC	Q10572;		
DT	09-APR-1991	(first entry)	
DE	Human Natriuretic Peptide Receptor B.		
KE	NPBR; ANP; BNP; CNP; kidney failure; heart failure; protein kinase;		
KW	hyperaldosteronism; glaucoma; guanyl cyclase.		
OS	Homo sapiens.		
FH	Key	Location/Qualifiers	
FT	Peptide	1..22	
FT	/label=	signal sequence	
FT	Protein	12	
FT	/label=	mature NPBR	
FT	Domain	23..455	
FT	/label=	extracellular domain	
FT	/note=	"binds natriuretic peptides A, B and C]"	
FT	Domain	456..456	
FT	/label=	transmembrane domain	
FT	Domain	479..1047	
FT	/label=	cytoplasmic domain	
FT	/note=	"GC and protien kinase activity"	
FT	Modified -site	24..26	
FT	/label=	N-glycos site	
FT	Modified -site	35..37	
FT	/label=	N-glycos site	

PD 11-DEC-1985.
 PR 17-MAY-1985; 105750.
 PA (SEAR) SEARLE G D & CO.
 PI Bell LD, Boseley PG, Porter AG;
 DR WPI; 85-311944/50.
 DR P-PSDB; P50033.
 PT New modified human beta interferon polypeptide(s) - prepd. by
 PT plasmid transformed bacteria, with improved antiviral,
 PT anti-proliferative and immune regulating actions
 PS Claim 28; Chart 21, page 43; 71pp; English.
 CC Compared with interferon beta prep. by recombinant methods, the
 CC INFs of the invention are more active and have different affinities
 CC for cell surface receptors (allowing selective targeting); they
 CC have higher therapeutic index; improved stability against microbial
 CC breakdown during synthesis; and better in vivo solubility and
 CC stability. They are also easier to recover from incubation mixts.
 SQ Sequence 498 BP; 112 A; 30 C; 68 G; 77 T;
 Query Match 6.9%; Score 51; DB 3; Length 498;
 Best Local Similarity 8.0%; Pred. No. 7.88e-05;
 Matches 39; Conservative 181; Mismatches 265; Indels 2; Gaps 2;
 Db 10 aayvtbqgnttytbcarmgdmnnaayttycarwnncaraaytbytbqggcar 69
 Cp 580 ARTCRITTYTHCANARNGYTCATATRTCTRTCTRTCTRTCTRTCTRTCTRTCT 521
 Db 70 ybaayggmgdytbgartaygytbaargaymgdgcngayt-tyaaratthccnctgga 128
 Cp 520 CYTCRCANACYTTCGNGCYTCCTGCTGCGNGCNGCNGNARARTCTCNWSNCGNARNG 461
 Db 129 ratcagncaraargarttycaraargaygngcnytbacnathtayaratybtca 188
 Cp 460 GNATRCANARRTCTRTCTGNGRAANCKRTCRCACTCN-ARCATRTCGGCCANGGR 402
 Db 189 raayathtygcnathtymgdcargywnwnnncnngntggaaygaracnathgt 248
 Cp 401 AANCCRANGCNCATNACNGCGCCANCKRCYTTNACTYGNACRCANARNSRTGR 342
 Db 249 ngaraaytbytbgcnaaygntaycaycarathaaycaytbaaarcngntytbgarga 308
 Cp 341 CANGGYTGNATNGYTCRTCNARRTCTCNARRCANACNGCGCRAANARNSRCANARR 282
 Db 309 raarytbgaargargaytyacnmgdgnaarytbatqwnwnnnytbcaaytbaarmg 368
 Cp 281 AAYTTYTNGTTCGRTGRCAYTGYTTTCATNACNARNGNATCCANGCNGCYTYG 222
 Db 369 dtaayvgmgdathytbcaytavytbaargcnaargartaywnncaytygngntggac 428
 Cp 221 TGNARNACYTCTTCATNGYTCRTGCGNARNAARRTTNGGNARCKCATRTTYTGTAY 162
 Db 429 nathgtmgdgtngarathytbmddayttytatyvathaaaymgdytbacngntayt 488
 Cp 161 TGNATNCCTGRCANARYTGNARRTTNGCGNATNGCGYTCARTTNSNCKYTTTAN 102
 Db 489 bmgdaay 495
 Cp 101 WSRART 95
 RESULT 8
 ID N50023 standard; DNA; 501 BP.
 AC N50023;
 DT 04-SEP-1991 (first entry)

DE Sequence encoding new modified human beta interferon polypeptides
 DE IFNX 416.
 KW Antiviral; cell growth regulator; immune system regulator;
 KW antiproliferative; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..501
 PN EP-163993-A.
 PD 11-DEC-1985.
 PR 17-MAY-1985; 105750.
 PR 17-MAY-1984; GB-012564.
 PA (SEAR) SEARLE G D & CO.
 PI Bell LD, Boseley PG, Porter AG;
 DR WPI; 85-311944/50.
 DR P-PSDB; P50022.
 PT New modified human beta interferon polypeptide(s) - prepd. by
 PT plasmid transformed bacteria, with improved antiviral,
 PT anti-proliferative and immune regulating actions
 PS Claim 28; Chart 2a, page 32; 71pp; English.
 CC Compared with interferon beta prep. by recombinant methods, the
 CC INFs of the invention are more active and have different affinities
 CC for cell surface receptors (allowing selective targeting); they
 CC have higher therapeutic index; improved stability against microbial
 CC breakdown during synthesis; and better in vivo solubility and
 CC stability. They are also easier to recover from incubation mixts.
 SQ Sequence 501 BP; 107 A; 31 C; 69 G; 80 T;
 Query Match 6.9%; Score 51; DB 3; Length 501;
 Best Local Similarity 16.0%; Pred. No. 7.88e-05;
 Matches 50; Conservative 95; Mismatches 167; Indels 1; Gaps 1;
 Db 166 gonytbacnathtaygaratgytbcaraayathtygcnathtymgdcargaywnwnn 225
 Cp 470 SNWSNGAYCAYYTYTNCNGCNCACNGARGCNCNAARCTNTGYGARGCNTGYAARA 529
 Db 226 wnnacngntggaaygaracnathgtngaraaytbytbqcnnaaygnt-taycaycarat 284
 Cp 530 AYARAAYCAYGAYGAAYAYATNATGARGACNNTYNTGYAARAAYGATTYGCNTYNA 589
 Db 285 haaycayvtbaarcngntytbgargataarytbgaraargaytyacnmgdgnaa 344
 Cp 590 ARATNAARCTNAARFARATNACNTAYATNAAYMGNGAYACNAARATNATNTYNGARACNA 649
 Db 345 rytbatqwnwnnnytbcaaytbaarmgdtaytayggmgdathytbcaytatybaargc 404
 Cp 650 ARWSNAARACNATNTAYARYTNAAYGNGNTWSNGARMGNGAYTYTNAARAARWSNGNTNY 709
 Db 405 naargattaywnncaytygcntggacnathgtmgdgtngarathytbmddaytyta 464
 Cp 710 TNYTGGYTNARCAWNSNYTNCARTGYACNTGYGARGARATGAAYGAYATNAAYGCNCNT 769
 Db 465 ytyathaaaymgd 477
 Cp 770 AYYTNGTNAATGGG 782
 RESULT 9
 ID N50028 standard; DNA; 501 BP.
 AC N50028;
 DT 04-SEP-1991 (first entry)
 DE Sequence encoding new modified human beta interferon polypeptides
 DE IFNX 445.
 KW Antiviral; cell growth regulator; immune system regulator;

Cp 308 CANACNGCGCAARNAARNAARFAAYT 278

RESULT 11

ID N50023 standard; DNA; 501 BP.
AC N50023;
DT 04-SEP-1991 (first entry)
DE Sequence encoding new modified human beta interferon polypeptides
DE IFNX 416.
KW Antiviral; cell growth regulator; immune system regulator;
KW antiproliferative; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..501
FT /*tag= a
FN EP-163993-A.
PD 11-DEC-1985.
PF 17-MAY-1985; 105750.
PR 17-MAY-1984; GB-012564.
PA (SEAR) SEARLE G D & Co.
PI Bell ID, Boseley PG, Porter AG;
WPI; 85-311944/50.
DR P-PSDB; P50022.
PT New modified human beta interferon polypeptide(s) - prepd. by
PT plasmid transformed bacteria, with improved antiviral,
PT anti-proliferative and immune regulating actions
PS Claim 28; Chart 2a, page 32; 71pp; English.
CC Compared with interferon beta prepd. by recombinant methods, the
CC INFs of the invention are more active and have different affinities
CC for cell surface receptors (allowing selective targeting); they
CC have higher therapeutic index; improved stability against microbial
CC breakdown during synthesis; and better in vivo solubility and
CC stability. They are also easier to recover from incubation mixts.
SQ Sequence 501 BP; 107 A; 31 C; 69 G; 80 T;

Query Match 6.8%; Score 50; DB 3; Length 501;

Best Local Similarity 14.9%; Pred. No. 1.54e-04;

Matches 68; Conservative 138; Mismatches 246; Indels 4; Gaps 3;

Db 48 twnccaraarytbybtggcarytbmnyggmgdytbgartaytgytbaargaymgdca 107

Cp 733 ATGNARNSRCTYTNARCCANARNACNSYTYTNNARRTCNCKYTCNWSNACNCRT 674

Db 108 ygytygnttyccncargarttygaygnaaycarttycargaargaygngc 167

Cp 673 TNARYTTRTANATNGYTTNWSYTTNGYTCNARNATNATYTTNGTRTCNCKRTTNATRT 614

Db 168 nytbacnathaygaratgytbcaraayathtgycnathtymgdccargaywnwnwn 227

Cp 613 ANGNATYTCYTNACTYTNATYTNARNCCRAARTCRITYTTRCANARNGYTCATNA 554

Db 228 hacngntggaaygaracnathgtngraaaytbytbqnaaygntaycaycarathaa 287

Cp 553 TRTCRTTRTCRTCTRTYTTTNTYTRCANGCYTCRCANACYTNGGNGCYTCYTCNG 494

Db 288 ycytybaarcnctnytbqargata--arytbqaraa--rgargaytyacmgdgnaa 344

Cp 493 TNGCGNARNARRTGTCTNWSNSNCNARNGGNATRCANARRTCRTTCYTCNGGGA 434

Db 345 rytbatgwnwnnytbcaaytbaarmgdtaytayggmgdathytcaytaytbaargc 404

Cp 433 ANCKRTGCAYTCNARCATRTCTGCGCCAGCAACCCRAANGCNWSCATNACNGCGC 374

Db 405 naargattaywnncaytgycntggacnathgtnmgdgtngarathytbmgdaaytyta 464

Cp 373 ANCKRTCYITNACTYTCNACRCANARNWSRTGRCANGCYTCNATNGYTCRTCNARRTCRT 314

Db 465 ytyythaaymgdytbacngngntay-ytbmgdaayt 499

Cp 313 CNARRCANACNGCGCAARNAARNAARNAARFAAYT 278

RESULT 12

ID N50029 standard; DNA; 501 BP.
AC N50029;
DT 04-SEP-1991 (first entry)
DE Sequence encoding new modified human beta interferon polypeptides
DE IFNX 446.
KW Antiviral; cell growth regulator; immune system regulator;
KW antiproliferative; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..501
FT /*tag= a
FN EP-163993-A.
PD 11-DEC-1985.
PF 17-MAY-1985; 105750.
PR 17-MAY-1984; GB-012564.
PA (SEAR) SEARLE G D & Co.
PI Bell ID, Boseley PG, Porter AG;
WPI; 85-311944/50.
DR P-PSDB; P50028.
PT New modified human beta interferon polypeptide(s) - prepd. by
PT plasmid transformed bacteria, with improved antiviral,
PT anti-proliferative and immune regulating actions
PS Claim 28; Chart 2g, page 38; 71pp; English.
CC Compared with interferon beta prepd. by recombinant methods, the
CC INFs of the invention are more active and have different affinities
CC for cell surface receptors (allowing selective targeting); they
CC have higher therapeutic index; improved stability against microbial
CC breakdown during synthesis; and better in vivo solubility and
CC stability. They are also easier to recover from incubation mixts.
SQ Sequence 501 BP; 112 A; 31 C; 69 G; 79 T;

Query Match 6.8%; Score 50; DB 3; Length 501;

Best Local Similarity 16.0%; Pred. No. 1.54e-04;

Matches 72; Conservative 133; Mismatches 242; Indels 4; Gaps 3;

Db 53 araarytbybtggcarytbaayggmgdytbgartaytgytbaargaymgdatgaayt 112

Cp 728 ARNSRCTYTNARCCANARNACNSYTYTNNARRTCNCKYTCNWSNACNCRTTNARY 669

Db 113 tyggnathcngargatgarathacargcncarttycargaargaygngcnybba 172

Cp 653 TTRTANATNGYTTNWSYTTNGYTCNARNATNATYTTNGTRTCNCKRTTNATRTANGTN 609

Db 173 cnathaygaratgytbcaraayathtgycnathtymgdccargaywnwnwnnaacng 232

Cp 608 ATYTCYTNACTYTNATYTNARNCCRAARTCRITYTTRCANARNGYTCATNATRTCT 549

Db 233 gntggaaygaracnathgtngraaaytbytbqnaaygntaycaycarathaaaycay 292

Cp 548 TTRTCRTCTRTCTRTYTTTNTYTRCANGCYTCRCANACYTNGGNGCYTCYTCNGTNGCN 489

Db 293 tbaarcngntnytbqargata--arytbqaraa--rgargaytyacmgdgnaaaybba 349

Cp 488 GGNARNARRTCRTNWSNSNCNARNGGNATRCANARRTCRTTCYTCNGGRAANGCR 429

Db 350 tqwnwnybtcaaytbaarmgdtaytvggmngdathytbcaytbytbaargcnaarg 409
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Cp 428 TCRCAITNACATRTTCGCCGACGACRAANCCRAANGCNWSCATNACNGNGCRANCKR 369
Db 410 artatwnncaytvgcgtgacnathgtmgdgtngarathytbmgaaytbytta 469
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Cp 368 TCTTINACTGNACRCANRNWRSRTGRCANGGYTGNATNGTTCRTCNARTCRCTNARR 309
Db 470 thaaymgdytbaengngtay-ytbgmdaayt 499
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Cp 308 CANACNGCGCRAANRNWRSRCANARBAAYT 278

RESULT 13
ID N50024 standard; DNA; 501 BP.
AC N50024;
DT 04-SEP-1991 (first entry)
DE Sequence encoding new modified human beta interferon polypeptides
DE IFNX 417.
KW Antiviral; cell growth regulator; immune system regulator;
KW antiproliferative; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..501
FT /*tag= a
FN EP-163993-A.
PD 11-DEC-1985.
PF 17-MAY-1985; 105750.
PR 17-MAY-1984; GB-012564.
PA (SEAR) SEARLE G D & CO.
PI Bell LD, Boseley PG, Porter AG;
DR WPI; 85-311944/50.
DR P-PSDB; P50023.
PT New modified human beta interferon polypeptide(s) - prepd. by
PT plasmid transformed bacteria, with improved antiviral,
PT anti-proliferative and immune regulating actions
PS Claim 28; Chart 2b, page 33; 71pp; English.
CC Compared with interferon beta prepd. by recombinant methods, the
CC INFs of the invention are more active and have different affinities
CC for cell surface receptors (allowing selective targeting); they
CC have higher therapeutic index; improved stability against microbial
CC breakdown during synthesis; and better in vivo solubility and
CC stability. They are also easier to recover from incubation mixts.
SQ Sequence 501 BP; 110 A; 32 C; 66 G; 81 T;

Query Match 6.7%; Score 49; DB 3; Length 501;
Best Local Similarity 16.0%; Pred. No. 2.99e-04;
Matches 50; Conservative 94; Mismatches 168; Indels 1; Gaps 1;
Db 166 gcnbtacnathaygaratytbcaraaythtgygnathtymgdcaargaywnwn 225
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Cp 470 SNWSNGAYCAYTYNWCNCNACARGARGCNCNCAARNTNGYRGANGGTGAARA 529
Db 226 wnnacngngtgaaygaracnathgtngaraaytbytbgcnaaygtnt-taycaycarat 284
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Cp 530 AYAAARAAYGAYGAYAYGAYATNATGACACNYTNTGYAARAAYCAYTYGCVYNA 589
Db 285 haaycaytbaarcngntytbgaraarytbgaraargaytyacmgdgnaa 344
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Cp 590 ARATNARGTNARGARATNACNTAYATNAYGNGAYACNARATNATNYNGARACNA 649
Db 345 rytbatgwnwnybtcaaytbaarmgdtaytvggmngdathytbcaytbytbaatgc 404
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Cp 650 ARWSNARACNATNATAYARTNAYGNGTNGWNGMNGGAYTYNARARWNSGNTY 709

Db 405 naargattaywncattvgcgtgacnathgtmgdgtngarathytbmgaaytbytta 464
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Cp 710 TWTGGYTNAARGATWSYNTNCARTGYACNTGYGARGARATGAAYGAYATNAYGCNCNT 769
Db 465 ytythaaymgd 477
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Cp 770 ATNGTNGTNGGG 782

RESULT 14
ID N50032 standard; DNA; 501 BP.
AC N50032;
DT 04-SEP-1991 (first entry)
DE Sequence encoding new modified human beta interferon polypeptides
DE IFNX 449.
KW Antiviral; cell growth regulator; immune system regulator;
KW antiproliferative; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..501
FT /*tag= a
FN EP-163993-A.
PD 11-DEC-1985.
PF 17-MAY-1985; 105750.
PR 17-MAY-1984; GB-012564.
PA (SEAR) SEARLE G D & CO.
PI Bell LD, Boseley PG, Porter AG;
DR WPI; 85-311944/50.
DR P-PSDB; P50031.
PT New modified human beta interferon polypeptide(s) - prepd. by
PT plasmid transformed bacteria, with improved antiviral,
PT anti-proliferative and immune regulating actions
PS Claim 28; Chart 2j, page 41; 71pp; English.
CC Compared with interferon beta prepd. by recombinant methods, the
CC INFs of the invention are more active and have different affinities
CC for cell surface receptors (allowing selective targeting); they
CC have higher therapeutic index; improved stability against microbial
CC breakdown during synthesis; and better in vivo solubility and
CC stability. They are also easier to recover from incubation mixts.
SQ Sequence 501 BP; 108 A; 30 C; 72 G; 79 T;

Query Match 6.7%; Score 49; DB 3; Length 501;
Best Local Similarity 15.3%; Pred. No. 2.99e-04;
Matches 69; Conservative 135; Mismatches 243; Indels 4; Gaps 3;
Db 53 araarytbytbgcarytbaayggmgdytbgartaytgytbaargaymgdcaygayt 112
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Cp 728 ARNWSRTCTTNARCANARNACNWSYTTTNNARRTCNCKRYTCNWSNACNCRNTNARY 669
Db 113 tygnttyccngngargarttygaygnaaycarttycaraargaygngcnybta 172
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Cp 668 TTRTANATNGYTTNWSYTTNGTYCNARNATNATYTTNGTTCNCKRTTNATRTANGTN 609
Db 173 cnathaygaratytbcaraaythtgygnathtymgdcaargaywnwnwnnaeng 232
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Cp 608 ATYTCYTHACTYTNATYTTNARNGCRAARTCRITTYTTRCANARNGYTTCATNATRTCR 549
Db 233 gntggaaygaracnathgtngaraaytbytbgcnaaygtntaycaycarathaaycay 292
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Cp 548 TTRTCRTCTCRITTYTTRITTYTTCANGCYTCRCANACYTTNGNGCYTCYCNCNGCN 489
Db 293 tbaaracnntytbgargara--arytbgaraa--rgargaytyacmgdggnaarytba 349
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : :

Cp	488	GGNARNARTGTCNNWSNWSGNARNNGGNATCCANARRTCRTTRTCYTCNGGGRANCKR	429
Db	350	tgwnwnmytbcaytbbaargdtaiyayggmgdathytbcaytaytbbaargcnaarg	409
Cp	428	TCRCAYTCNARCATRTCNGGCCANGGRAANCRAAGCNWSCATNACNGGRCRANCKR	369
Db	410	artaywncaiygyctggacnathgtmgdgtngarathybmgdaaytytya	469
Cp	368	TCTTNACYTCNARCANARWWSRTRCANGGYTCNATGTTCTCTCNARRTCRTCNARR	309
Db	470	thaaymgdytbacngntay-ytbmgdaayt	499
Cp	308	CANACNGGCGRAANARWWSRANARRAAYT	278

RESULT	15	
ID	N50025 standard; DNA;	501 BP.
AC	N50025;	
DT	04-SEP-1991	(first entry)
DE	Sequence encoding new modified human beta interferon polypeptides	
DE	IFN γ 418.	
KW	Antiviral; cell growth regulator; immune system regulator;	
KW	antiproliferative; ss.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	CDS	1..501
FT	/tag= a	
PN	EP-163993-A.	
PD	11-DEC-1985.	
PF	17-MAY-1985;	105750.
PR	17-MAY-1984; GB-012564.	
PA	(SEAR) SEABLE G D & CO.	
PI	Bell LD, Boseley PG, Porter AG;	
DR	WPI; 85-311944/50.	
DR	P-PsDB: P50024.	

New modified human beta interferon polypeptide(s) - prepd. by
 plasmid transformed bacteria, with improved antiviral,
 anti-proliferative and immune regulating actions
 Claim 28; Chart 2c, page 34; 71pp; English.
 Compared with interferon beta prepd. by recombinant methods, the
 INFs of the invention are more active and have different affinities
 for cell surface receptors (allowing selective targeting); they
 have higher therapeutic index; improved stability against microbial
 breakdown during synthesis; and better in vivo solubility and
 stability. They are also easier to recover from incubation mixts.
 Sequence 501 BP; 112 A; 30 C; 69 G; 85 T;

Query Match 6.7%; Score 49; DB 3; Length 501;
Best Local Similarity 15.7%; Pred. No. 2.99e-04;
Matches 71; Conservative 134; Mismatches 242; Indels 4; Gaps 3;

53	araarytbybtgcgcaarytbaayggmgdytbgartaytgyybtbaatgaymgdatgaayt	112
	: : : : : : : : : : : : : : :	
728	ARNWERTCTTNARCCNARNWACNWSYTTTNNARBTCKYTCNWSNACNCRRTNARY	669
113	tygavathcncatgargarttygavggnaaycarttycaraagargaygcngcnybta	172
	: : : : : : : : : : : : : : :	
668	TTRTANATNGTNTNWSYTTNGTTCNARNATNATYTTNGTTRCNCKRTNATRTANGTN	609
173	cnaththaygaratgytbeataayathttvgcnaththtmgdcatgaywnwnwnnaacng	232
	: : : : : : : : : : : : : : :	
608	ATYTCYTTCNACYTNNATYTTNWRNGCRAARTCTTYTTCANARNGTYTCCATNATR	549
233	qntgaaaygaracnathdntdataaaytvtbqcnaaaydnttvcaycarathaaycayv	292

Cp	548	TTRTCRTCRITTYTTRTTCRCANGCYTCRCANACYTTNGGNGCYTCYTONGTNGCN	489
Db	293	tbaaraangntnytbearara--arytbgaraa-rgarqarttyvacnmddgnaarytba	349
Cp	488	GGVARNARRTRGTCNWSNWSGNCNARNGATRCANARTRCTRTTCYTNGGRCANCKR	429
Db	350	tgwnwnnytbcaaytbearmgdrtaytvggmddgathytbcaytaytvtbaargcnaatg	409
Cp	428	TGCATYCNARCATRTCTGCGCCGANGRAANCRAANGCNWSCATNACNGGRCANCKR	369
Db	410	artaywnncatgygntggacnathgtmgdgtngdarathybmgdaayttaytyta	469
Cp	368	TCYTINACYTCGNACRCANARNWSRTGRANGGYTGATNGYTCRTCNARRCTCNCARR	309
Db	470	thaaymgdytbacngntay--ytbmgdaayt	499
Cp	308	CANACNGGNCANARNWSCANARRAAYT	278

Search completed: Tue Dec 9 09:10:39 1997
Job time : 282 secs.